

STIC-Biotech/ChemLib

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Subject:

Jiang, Dong  
Friday, January 10, 2003 6:05 PM  
STIC-Biotech/ChemLib  
09/931,836

84042  
Priority RECEIVED 3/1/00 (PCT)  
JAN 13 2003 8/16/01 (FD)

Please search 1) SEQ ID NO:2

-issued  
-commercial

Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).  
Thank you very much.

Dong Jiang (78243)  
703-305-1345  
U.S. Patent and Trademark Office  
Art Unit 1646  
dong.jiang@uspto.gov  
CM1-10D08  
Mail stop: CM1-10D19

STIC Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 1/13  
Date Completed: 1/14  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:31:23 : Search time 36 Seconds  
(without alignments)  
910.546 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLWRQLIYWOLLALFLPFC.....LHGDRHQRSTFAGFLIFETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_101002.\*  
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1367	100.0	246	21	Human Immune syste
2	1367	100.0	246	21	Human adipocyte co
3	1367	100.0	246	21	A novel polypeptid
4	1367	100.0	246	22	Human membrane or
5	1367	100.0	246	23	Novel human secret
6	1320.5	96.6	319	23	Novel human secret
7	1311	95.9	246	21	Mouse zacrip2 prote
8	1208	88.4	225	22	Human polypeptide
9	884	64.7	202	22	Human polypeptide
10	792.5	58.0	223	22	Human protein havi

11	721	52.7	128	20	AAV11485	Human 5' EST seque
12	663	48.5	126	22	AA40074	Human polypeptide
13	582	42.6	105	21	AA75969	Rat skin cell prot
14	582	42.6	105	21	AA75969	Rat skin cell prot
15	582	42.6	105	22	AA55908	Skin cell protein,
16	582	42.6	105	22	AA55908	Skin cell protein,
17	582	42.6	105	22	AA55964	Rat protein isolat
18	582	42.6	105	23	AB72108	Rat protein isolat
19	325	23.8	267	23	AAU84378	Novel human secret
20	319	23.3	285	21	AA76103	Rat skin cell secr
21	319	23.3	285	22	AA56042	Skin cell protein,
22	319	23.3	285	23	AB72242	Rat protein isolat
23	316	23.1	294	21	AA76039	Rat skin cell prot
24	316	23.1	294	22	AA55978	Skin cell protein,
25	316	23.1	294	23	AB72178	Rat protein isolat
26	315.5	23.1	288	22	AAE09443	Human SHACRP30a p
27	315	23.0	289	23	ABG66742	Human novel polype
28	315	23.0	289	23	ABP61017	Novel human protei
29	315	23.0	296	23	AAO15424	Human ganset metab
30	315	23.0	303	22	AAE09444	Human SHACRP30a p
31	315	23.0	303	22	AA50371	Human ZACRP7, Hom
32	313	22.9	285	21	AA37344	Murine ACRF30R1M.
33	309	22.6	289	22	AA50376	Mouse ZACRP7, Mus
34	308	22.5	289	23	AB72306	Rat protein isolat
35	306	22.4	314	23	ABP41487	Human ovarian anti
36	306	22.4	331	22	AAU19557	Human diagnostic a
37	304	22.2	285	21	AA30232	Human adipocyte co
38	304	22.2	285	21	AA54321	A polypeptide desi
39	304	22.2	285	22	AA50374	Human adipocyte co
40	297.5	21.8	225	23	AB80583	Human sbg103026C1
41	297.5	21.8	244	18	AAW09108	Human adipocyte co
42	296.5	21.7	260	21	AAV91522	Human secreted pro
43	296.5	21.7	287	21	AAV91666	Human secreted pro
44	294	21.5	247	18	AAW09107	Murine adipocyte c
45	294	21.5	247	22	AAE05528	Mouse OBG3 protein

#### ALIGNMENTS

RESULT 1

AA15548

ID AA15548 standard; Protein; 246 AA.

XX AA15548;

AC AA15548;

XX 28-FEB-2001 (first entry)

DT Human immune system molecule from Incyte clone 1890540.

XX Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;

XX Anti-inflammatory; keratolytic; anti-HIV; anti-allergic; antianemic;

KW antiarteriosclerotic; antidiabetic; antidiabetic; antidiabetic; cancer;

KW antiarthritic; dermatological; antithyroid; virucide; hepatotropic; antibody;

KW immunosuppressive; cytostatic; fungicide; protozoacide; antibacterial;

KW gene therapy; diagnostic; immunological disorder; viral infection;

KW bacterial infection; fungal infection; parasitic infection; immunogen.

XX Homo sapiens.

OS WO2000060080-A2.

PN 12-OCT-2000.

PD 04-APR-2000; 2000WO-US09072.

XX 05-APR-1999; 99US-0127852.

PR 05-MAY-1999; 99US-0132647.

XX (INCY-) INCYTE PHARM INC.

PA Yue H, Lal P, Tang Y, Baughn MR, Azimzai Y, Lu DAM;

XX WPI; 2000-665005/64.

XX WPI; 2000-665005/64.

DR WPI; 2000-665005/64.

DR N-PSDB; AAA95787.  
XX New human immune system molecules 1-15 and polynucleotides encoding  
PT them useful for diagnosing, treating or preventing e.g. immunological  
PT disorders, infections, cell proliferative disorders, microbial  
PT infections -  
XX  
XX  
XX Claim 1; Page 85; 95pp; English.  
XX  
XX This sequence represents a human immune system molecule (IMOL) encoded  
CC by the cDNA isolated as clone 1890540 from the Incyte BLADU707 library.  
CC The human IMOLs (AAB15536-B15550) and their encoding polynucleotides  
CC (AAA95775-A95789), and compositions comprising them are useful for the  
CC diagnosis, treatment or prevention of immunological disorders,  
CC infections and cell proliferative disorders, including cancer. The IMOL  
CC may be used to treat or prevent disorders associated with decreased  
CC expression or activity of IMOL, such as immunological disorders  
CC (e.g. inflammation, actinic keratosis, AIDS, Addison's disease),  
CC haematopoietic cancer, infections caused by virus (e.g. adenovirus,  
CC parvovirus, coronavirus), bacteria (e.g. Staphylococcus, Streptococcus,  
CC Shigella), fungi (e.g. Aspergillus, Blastomyces), parasites (e.g.  
CC Plasmodium, Trypanosoma, intestinal protozoa), cell proliferative  
CC disorders (e.g. actinic keratosis, arteriosclerosis, bursitis), and  
CC cancers (e.g. leukemia, melanoma, sarcoma). The peptides are also  
CC useful as immunogens for the development of antibodies that  
CC specifically recognize these peptides. The polynucleotides may be used  
CC to detect and quantify gene expression in biopsied tissues in which  
CC expression of IMOL may be correlated with the disease, as targets in a  
CC microarray, to detect differences in gene sequences among normal,  
CC carrier and affected individuals, and for screening libraries of  
CC compounds in drug screening techniques. Antibodies which specifically  
CC bind to IMOL may be used for the diagnosis of disorders characterized  
CC by expression of IMOL, or in assays to monitor patients being treated  
CC with IMOL or agonists, antagonists, or inhibitors of IMOL.  
XX  
XX Sequence 246 AA;

Query Match 100.0%; Score 1367; DB 21; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2e-124;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MLWRQLIYWQLLALFFLPCLCODEYMESPTGGLPPDCSKCHGYSFRGYGPPGPG 60  
  
QY 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120  
DB 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120  
  
QY 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRFGAPVSGVYFFTFSSMMKHEDVEEYV 180  
DB 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRFGAPVSGVYFFTFSSMMKHEDVEEYV 180  
  
QY 181 YLMHNGNTVFSMYSYEMKGSKDSSTSSNAVLKLAGDEVWLMRGMNGALHGDHQRFSFAGF 240  
DB 181 YLMHNGNTVFSMYSYEMKGSKDSSTSSNAVLKLAGDEVWLMRGMNGALHGDHQRFSFAGF 240  
  
QY 241 LLFETK 246  
DB 241 LLFETK 246

RESULT 2  
ID AAB29580  
XX AAB29580 standard; Protein; 246 AA.  
AC AAB29580;  
XX  
XX 19-FEB-2001 (first entry)  
DT  
XX Human adipocyte complement related protein homologue zacrp3, SEQ ID NO:2.  
DE  
XX Human zacrp3; adipocyte complement related protein homologue;  
KW

KW ACRP30; C1q domain; collagen-like domain; energy balance modulation;  
KW cellular metabolism; metabolic disorder; obesity; anorexia;  
KW antimicrobial agent; infection; platelet aggregation inhibition;  
KW adhesion; activation; vascular injury; antibacterial; antiviral.  
XX  
OS Homo sapiens.  
XX  
PN WO200063377-A1.  
XX  
XX 26-OCT-2000.  
XX  
PF 19-APR-2000; 2000WO-US10454.  
XX  
PR 20-APR-1999; 99US-0294943.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Piddington CS, Bishop PD;  
XX WPI; 2000-665243/64.  
XX N-PSDB; AAC64058.  
  
PT Novel zacrp3 polypeptides used to treat or prevent bacterial or viral  
PT infections, for wound healing, improving blood flow, and to analyze  
PT energy efficiency in mammals -  
XX  
PS Claim 2; Page 109-110; 123pp; English.  
XX  
CC The invention relates to the human zacrp3 protein (AAB29580) and to  
CC nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homologue  
CC of adipocyte complement related protein (ACRP30) and contains a  
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a  
CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is  
CC located on chromosome 5p12. The invention also relates to zacrp3  
CC fragments, fusion proteins containing zacrp3 polypeptides,  
CC zacrp3-specific antibodies, expression constructs and host cells  
CC comprising zacrp3 nucleic acids, and methods of recombinant production of  
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the  
CC study and modulation of cellular metabolism and energy balance in  
CC mammals, and may therefore be used to treat disorders such as obesity and  
CC anorexia, and conditions associated with these disorders. Due to its C1q  
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful  
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious  
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion  
CC proteins, antibodies and activity modulators may also be used to inhibit  
CC collagen-induced platelet aggregation, adhesion, or activation, and may  
CC therefore have potential for promoting blood flow within the vasculature  
CC of a mammal e.g., to treat injury to the vasculature or other collagenous  
CC tissue. Human zacrp3 and its antibodies may additionally be used to study  
CC dimerisation and oligomerisation. The present sequence represents human  
XX zacrp3.  
SQ Sequence 246 AA;

Query Match 100.0%; Score 1367; DB 21; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2e-124;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MLWRQLIYWQLLALFFLPCLCODEYMESPTGGLPPDCSKCHGYSFRGYGPPGPG 60  
  
QY 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120  
DB 61 PPGIPGNHNGNNGATGHEGAKGKGDGLGPRGERGQHGPKGKGYGPIPELQIAF 120  
  
QY 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRFGAPVSGVYFFTFSSMMKHEDVEEYV 180  
DB 121 MASLATHFSNQNSGIIFSSSVETNIGNFFDVTMTGRFGAPVSGVYFFTFSSMMKHEDVEEYV 180  
  
QY 181 YLMHNGNTVFSMYSYEMKGSKDSSTSSNAVLKLAGDEVWLMRGMNGALHGDHQRFSFAGF 240  
DB 181 YLMHNGNTVFSMYSYEMKGSKDSSTSSNAVLKLAGDEVWLMRGMNGALHGDHQRFSFAGF 240

Qy 241 LLFETK 246  
Db 241 LLFETK 246  
RESULT 3  
AAB18909  
ID AAB18909 standard; Protein; 246 AA.  
XX AAB18909;  
AC AAB18909;  
XX 08-FEB-2001 (first entry)  
XX A novel polypeptide designated PRO1484.  
XX Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;  
KW PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;  
KW PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5990; PRO6030;  
KW PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;  
KW insulinemia; kidney disorder; Bergers disease; nephropathy;  
KW Schonlein-Henoch purpura; celliac disease; dermatitis herpeticiformis;  
KW Crohns disease.  
XX Homo sapiens.  
XX Location/Qualifiers  
FH Key  
FT Peptide  
FT 1..22  
FT /note= "signal peptide"  
FT Domain  
FT 33..66  
FT /note= "Clq domain protein"  
FT Domain  
FT 42..75  
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FT Domain  
FT 45..78  
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FT Domain  
FT 48..81  
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FT /note= "Clq domain protein"  
FT Domain  
FT 235..244  
FT /note= "Clq domain protein"  
XX WO200056889-A2.  
XX 28-SEP-2000.  
XX 01-MAR-2000; 2000WO-US05601.  
XX 23-MAR-1999; 99US-0125774.  
XX 23-MAR-1999; 99US-0125778.  
XX 24-MAR-1999; 99US-0125826.  
XX 31-MAR-1999; 99US-0127035.  
XX 05-APR-1999; 99US-0127706.  
XX 21-APR-1999; 99US-0130359.  
XX 27-APR-1999; 99US-0131270.

PR 27-APR-1999; 99US-0131272.  
PR 27-APR-1999; 99US-0131291.  
PR 04-MAY-1999; 99US-0132371.  
PR 04-MAY-1999; 99US-0132379.  
PR 04-MAY-1999; 99US-0132383.  
PR 25-MAY-1999; 99US-0135750.  
PR 08-JUN-1999; 99US-0138166.  
PR 20-JUL-1999; 99US-0144791.  
PR 03-AUG-1999; 99US-0146970.  
PR 09-DEC-1999; 99US-0170262.  
XX (GETH ) GENENTECH INC.  
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2000-628263/60.  
DR N-PSDB; AAA96336.  
XX Novel secreted and transmembrane polypeptides useful for diagnosing  
PT tumour in a mammal, for identifying agonists and antagonists of the  
XX polypeptide and for therapeutic use -  
XX Claim 12; Fig 2; 222pp; English.  
XX The present sequence represents a secreted or transmembrane polypeptide.  
CC The specification describes polypeptides designated PRO1484, PRO4334,  
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,  
CC PRO4356, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,  
CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
CC useful for diagnosing tumour in a mammal. The polypeptides, their  
CC agonists and antagonists are useful treating a condition associated with  
CC expression or activity of the polypeptide. Conditions treated include  
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
CC capable of inducing proliferation of mammalian kidney mesangial cells  
CC and are therefore useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Bergers disease or other  
CC nephropathies associated with Schonlein-Henoch purpura, celliac disease,  
CC dermatitis herpeticiformis or Crohns disease. The nucleic acids may be used  
CC to generate transgenic animals for use in development and screening of  
CC therapeutically useful reagents and also for chromosome identification  
CC and tissue typing.  
XX SQ Sequence 246 AA:  
Query Match 100.0%; Score 1367; DB 21; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2e-124;  
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLWRQLIYWQLLALFFLPFCLCQDEYMESPTGGLPDCSKCCHGDYSFRGYQGP GPG 60  
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Db 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYPGIPPELQIAF 120  
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Db 181 YLMHNGNTVFSWYSEYEMKGS DTSNHA VLKLAGDVEWLRMGALHG DHRSTFAGF 240  
Qy 241 LLFETK 246  
Db 241 LLFETK 246  
RESULT 4  
AAB88447  
ID AAB88447 standard; Protein; 246 AA.

XX AAB88447;  
 AC 23-MAY-2001 (first entry)  
 DT Human membrane or secretory protein clone PSEC0232.  
 DE Human; secretory protein; membrane protein; vaccine; gene therapy;  
 XX rheumatoid arthritis; diabetes.  
 KW Homo sapiens.  
 OS EP1067182-A2.  
 XX 10-JAN-2001.  
 PN 07-JUL-2000; 2000EP-0114090.  
 XX 08-JUL-1999; 99JP-0194179.  
 PR 11-JAN-2000; 2000JP-0118775.  
 PR 02-MAY-2000; 2000JP-0183766.  
 XX (HELI-) HELIX RES INST.  
 PA Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;  
 PI WPI; 2001-093989/11.  
 XX N-PSDB; AAF93874.  
 DR Nucleic acids encoding secretory proteins/membrane proteins, useful in  
 PT gene therapy or as candidate target molecules in drug development -  
 XX Claim 1: SEQ ID 262; 609pp + CD ROM; English.  
 PS This invention relates to nucleic acid sequences AAF93744 - AAF93916  
 CC which encode human secretory or membrane proteins represented by  
 CC AAB88317 - AAB88419. Included in the invention are primers  
 CC cDNA sequences of the invention. The invention also includes methods for  
 CC the production of antibodies directed against the proteins, and cDNA  
 CC sequences, which can be used in vaccines. The polynucleotide sequences  
 CC can be used in gene therapy. The polynucleotide sequences and the  
 CC proteins they encode may be used in the prevention, treatment and  
 CC diagnosis of diseases associated with inappropriate secretion and  
 CC protein/membrane protein expression. The nucleic acids and complementary  
 CC sequences may also be used as DNA probes in diagnostic assays  
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the  
 CC presence of similar nucleic acid sequences in samples. They may also be  
 CC used to study the expression and function of secretory proteins/membrane  
 CC polypeptides and their role in metabolism. The polypeptides may be used  
 CC as antigens in the production of antibodies against them and in assays to  
 CC identify modulators (agonists and antagonists) of expression and  
 CC activity. The antibodies and antagonists may also be used as therapeutic  
 CC agents to down regulate expression and activity. The antibodies may also  
 CC be used as diagnostic agents for detecting the presence of the  
 CC polypeptides in samples (e.g. by enzyme linked immunosorbent assay  
 CC (ELISA)). Examples of diseases which may be treated include rheumatoid  
 CC arthritis and diabetes.  
 XX Sequence 246 AA;  
 SQ Query Match 100.0%; Score 1367; DB 22; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 2e-124;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MLWRQLIYQWLLALFPLPCLQDEYMESPTQGLPPDCSKCHGDSYPRGYPGPPPG 60  
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 DB 61 PPGIPGNHNNNGATGHEGAKGKGDGLGPRGEGHKGKGYGYPGPELQIAF 120

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 DB 121 MASLATHFSNQNSGIIFSSVETNIGNFFDVTGRFCAPYSGVYFFTFSMKKHDEVEYV 180  
 QY 181 YLMHNGNTVFSMYSEYMKGKSDTSSNHHAVLKLAKGDEVWLRMGNGALHGDHGFSTFAGF 240  
 DB 181 YLMHNGNTVFSMYSEYMKGKSDTSSNHHAVLKLAKGDEVWLRMGNGALHGDHGFSTFAGF 240  
 QY 241 LLFETK 246  
 DB 241 LLFETK 246  
 RESULT 5  
 AAU84371  
 ID AAU84371 standard; Protein; 246 AA.  
 XX AC AAU84371;  
 XX DT 08-MAY-2002 (first entry)  
 XX DE Novel human secreted or membrane-associated protein #10.  
 XX KW Human; secreted protein; membrane-associated protein; hypertension;  
 KW inflammatory disorder; neurological disorder; haematopoietic disorder;  
 KW skeletal developmental disorder; growth abnormality; autoimmune disorder;  
 KW neurodegenerative disorder; nervous system disorder; bacterial infection;  
 KW peripheral myelinopathy; viral infection; cancer; obesity; diabetes;  
 KW hypotension; sexual development disorder; blood disorder.  
 XX OS Homo sapiens.  
 XX PN WO200204600-A2.  
 XX PD 17-JAN-2002.  
 XX PF 12-JUL-2001; 2001WO-US21985.  
 XX PR 12-JUL-2000; 2000US-218033P.  
 XX PR 21-AUG-2000; 2000US-226517P.  
 XX PA (SMK ) SMITHKLINE BEECHAM CORP.  
 PA (SMK ) SMITHKLINE BEECHAM PLC.  
 XX (GLAX ) GLAXO GROUP LTD.  
 PI Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;  
 PI Smith RF, Xiang Z, Xie Q;  
 XX WPI; 2002-188468/24.  
 DR N-PSDB; ABK35591.  
 XX Novel secreted and membrane-associated polypeptides and polynucleotides  
 PT encoding the polypeptides, for preventing, treating and ameliorating  
 PT cancers, mental or sexual developmental disorders, and malignant tumours  
 PS Claim 1: Page 131-132; 151pp; English.  
 CC The present invention relates to the isolation of novel human secreted  
 CC or membrane-associated proteins and the genes encoding them. The  
 CC sequences of the invention are useful for treating, preventing and  
 CC ameliorating various diseases such as inflammatory disorders (e.g.  
 CC asthma), neurological disorders (e.g. dementia), haematopoietic  
 CC disorders, skeletal developmental disorders, growth abnormalities,  
 CC neurodegenerative disorders (e.g. Huntington's disease), nervous system  
 CC disorders, autoimmune disorders (e.g. rheumatoid arthritis),  
 CC peripheral myelinopathies, viral and bacterial infections,  
 CC alpha-mannosidosis, diabetes, cancers, malignant tumours, hyper- and  
 CC hypotension, obesity, bulimia, anorexia, manic depression, delirium,  
 CC mental retardation, Tourette's syndrome, schizophrenia, growth, mental  
 CC or sexual development disorders, and dysfunctions of the blood cascade  
 CC system including those leading to stroke. AAU84362-AAU84389 represent  
 CC the novel human secreted or membrane-associated proteins of the

```
CC  invention..
XX
SQ  Sequence      246 AA;

Query Match      100.0%; Score 1367; DB 23; Length 246;
Best Local Similarity 100.0%; Pred. No. 2e-124;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MLWRQLIYWQLLALFFLPFCQDEYMEPQTGGLPPDCSKCHGDSFRGYQGPYPGG 60
Dy  1 MLWRQLIYWQLLALFFLPFCQDEYMEPQTGGLPPDCSKCHGDSFRGYQGPYPGG 60
Qy  61 PPGIPGNHNGNNGATGHECAKGEKDGDLGPRGRGQHGPKGEKYPGIPPELQIAF 120
Dy  61 PPGIPGNHNGNNGATGHECAKGEKDGDLGPRGRGQHGPKGEKYPGIPPELQIAF 120
Qy  121 MASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKKHEDVEEYV 180
Dy  121 MASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTFSMKKHEDVEEYV 180
Qy  181 YLMINGNTVFSMYSYEMKGSDDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRSTFAGF 240
Dy  181 YLMINGNTVFSMYSYEMKGSDDTSSNHAVALKLAKGDEVWLRMGNGALHGDHQRSTFAGF 240
Qy  241 LLEFETK 246
Dy  241 LLEFETK 246

RESULT 6
AAU84370
ID  AAU84370 standard; Protein: 319 AA.
XX
AC  AAU84370;
XX
DT  08-MAY-2002 (first entry)
XX
DE  Novel human secreted or membrane-associated protein #9.
XX
KW  Human; secreted protein; membrane-associated protein; hypertension;
KW  inflammatory disorder; neurological disorder; haematopoietic disorder;
KW  skeletal developmental disorder; growth abnormality; autoimmune disorder;
KW  neurodegenerative disorder; nervous system disorder; bacterial infection;
KW  peripheral myelinopathy; viral infection; cancer; obesity; diabetes;
KW  hypotension; sexual development disorder; blood disorder.
XX
OS  Homo sapiens.
XX
PN  WO200204600-A2.
XX
PD  17-JAN-2002.
XX
PF  12-JUL-2001; 2001WO-US21985.
XX
PR  12-JUL-2000; 2000US-218033P.
XX
PR  21-AUG-2000; 2000US-226517P.
XX
PA  (SMIK ) SMITHKLINE BEECHAM CORP.
PA  (SMIK ) SMITHKLINE BEECHAM PLC.
XX  (GLAX ) GLAXO GROUP LTD.
XX
XX  Agarwal P, Cogswell JP, Lai Y, Martensen SA, Rizvi SK, Strum JC;
PI  Smith RF, Xiang Z, Xie Q;
XX
XX  WPI; 2002-188468/24.
DR  N-PSDB; ABK35590.
XX
PT  Novel secreted and membrane-associated polypeptides and polynucleotides
PT  encoding the polypeptides, for preventing, treating and ameliorating
PT  cancers, mental or sexual developmental disorders, and malignant tumours
XX
PS  Claim 1; Page 130-131; 151pp; English.

XX  The present invention relates to the isolation of novel human secreted
CC  or membrane-associated proteins and the genes encoding them. The
CC  sequences of the invention are useful for treating, preventing and
CC  ameliorating various diseases such as inflammatory disorders (e.g.
CC  asthma), neurological disorders (e.g. dementia), haematopoietic
CC  disorders, skeletal developmental disorders, growth abnormalities,
CC  neurodegenerative disorders (e.g. Huntington's disease), nervous system
CC  disorders, autoimmune disorders (e.g. rheumatoid arthritis),
CC  peripheral myelinopathies, viral and bacterial infections,
CC  alpha-mannosidosis, diabetes, cancers, malignant tumours, delirium,
CC  hypotension, obesity, bulimia, anorexia, manic depression, delirium,
CC  mental retardation, Tourette's syndrome, schizophrenia, growth, mental
CC  or sexual development disorders, and dysfunctions of the blood cascade
CC  system including those leading to stroke. AAU84362-AAU84389 represent
CC  the novel human secreted or membrane-associated proteins of the
CC  invention.
XX
SQ  Sequence      319 AA;

Query Match      96.6%; Score 1320.5; DB 23; Length 319;
Best Local Similarity 77.1%; Pred. No. 9.3e-120;
Matches 246; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

Qy  1 MLWRQLIYWQLLALFFLPFCQDEYMEP----- 28
Dy  1 MLWRQLIYWQLLALFFLPFCQDEYMEVSGRTNKVARIVOSHQQTGRSSRRREKVRER 60
Qy  29 -----SPQTGGLPPDCSKCHGDY 47
Dy  61 SHPKTGTVDNNTSTDLSLRPDELPHPEVDLDAQITTFWGOSPTGGLPPDCSKCHGDY 120
Qy  48 SFRGYQGPYPGGIPGNHNGNNGATGHEGAKGEKDGKDLGPRGRGQHGPKGEK 107
Dy  121 SFRGYQGPYPGGIPGNHNGNNGATGHEGAKGEKDGKDLGPRGRGQHGPKGEK 180
Qy  108 GYPGIPPELQIAFASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTF 167
Dy  181 GYPGIPPELQIAFASLATHFSNQNSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFTF 240
Qy  168 SMKKHEDVEEYVYLMHNGNTVFSMYSYEMKGSDDTSSNHAVALKLAKGDEVWLRMGNGAL 227
Dy  241 SMKKHEDVEEYVYLMHNGNTVFSMYSYEMKGSDDTSSNHAVALKLAKGDEVWLRMGNGAL 300
Qy  228 HGDHQRSTFAGFLLEFETK 246
Dy  301 HGDHQRSTFAGFLLEFETK 319

RESULT 7
AAB29582
ID  AAB29582 standard; Protein: 246 AA.
XX
AC  AAB29582;
XX
DT  19-FEB-2001 (first entry)
XX
DE  Mouse zacr2 protein, SEQ ID NO:12.
XX
KW  Mouse zacr2; adipocyte complement related protein homologue;
KW  ACRP30; C1q domain; collagen-like domain; energy balance modulation;
KW  cellular metabolism; metabolic disorder; obesity; anorexia;
KW  antimicrobial agent; infection; platelet aggregation inhibition;
KW  adhesion; activation; vascular injury; antibacterial; antiviral;
XX  human zacr3 homologue.
XX
OS  Mus musculus.
XX
PN  WO2000063377-A1.
XX
PD  26-OCT-2000.
XX
PF  19-APR-2000; 2000WO-US10454.
```

XX 20-APR-1999; 990S-0294943.  
PR (ZYMO ) ZYMOGENETICS INC.  
XX Piddington CS, Bishop PD;  
XX WPI; 2000-665243/64.  
DR N-PSDB; AAC64064.  
XX Novel zacrp3 polypeptides used to treat or prevent bacterial or viral  
PT infections, for wound healing, improving blood flow, and to analyze  
PT energy efficiency in mammals -  
XX Disclosure; Page 117-118; 123pp; English.  
PS The invention relates to the human zacrp3 protein (AAB29580) and to  
XX nucleic acids which encode it (AAC64058, AAC64063). Zacrp3 is a homologue  
XX of adipocyte complement related protein (ACRP30) and contains a  
CC collagen-like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a  
CC C-terminal C1q domain comprising 10 beta-strands. The zacrp3 gene is  
CC located on chromosome 5p12. The invention also relates to zacrp3  
CC fragments, fusion proteins containing zacrp3 polypeptides,  
CC zacrp3-specific antibodies, expression constructs and host cells  
CC comprising zacrp3 nucleic acids, and methods of recombinant production of  
CC zacrp3. Human zacrp3, and its agonists and antagonists may be used in the  
CC study and modulation of cellular metabolism and energy balance in  
CC mammals, and may therefore be used to treat disorders such as obesity and  
CC anorexia, and conditions associated with these disorders. Due to its C1q  
CC like domain, zacrp3 and zacrp3-containing fusion proteins may be useful  
CC as antimicrobial agents, promoting lysis or phagocytosis of infectious  
CC organisms such as bacteria or viruses. Zacrp3, its fragments, fusion  
CC proteins, antibodies and activity modulators may also be used to inhibit  
CC collagen-induced platelet aggregation, adhesion, or activation, and may  
CC therefore have potential for promoting blood flow within the vasculature  
CC of a mammal e.g., to treat injury to the vasculature or other collagenous  
CC tissue. Human zacrp3 and its antibodies may additionally be used to study  
CC dimerisation and oligomerisation. The present sequence represents mouse  
CC zacrp2, a homologue of human zacrp3.  
XX SQ Sequence 246 AA;  
Query Match 95.9%; Score 1311; DB 21; Length 246;  
Best Local Similarity 95.9%; Pred. No. 5.5e-119;  
Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MLNRQLIYWQLLALFLPFLCQDEYNESPTGGLPPDCSKCHGDSYFRGYGPPGPG 60  
Db 1 MLGRQRIWHLLPLFLPFLCQDEYNESPTAGGLPPDCSKCHGDSYFRGYGPPGPG 60  
QY 61 PPGIPGNHGNNGNATGHEGAKGKGDGLGRGERGHGPKGKGYPIPELQIAF 120  
Db 61 PPGIPGNHGNNGNATGHEGAKGKGDGLGRGERGHGPKGKGYPIPELQIAF 120  
QY 121 MASLATHFSNQNGIIFSSVETNIGNFDVMTGRFGAPSGVYFFTFSMKKHEDVEEYV 180  
Db 121 MASLATHFSNQNGIIFSSVETNIGNFDVMTGRFGAPSGVYFFTFSMKKHEDVEEYV 180  
QY 181 YLHNGNTVFSMYSYEMKGSQDSSSHAVLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGF 240  
Db 181 YLHNGNTVFSMYSYETKGSQDSSSHAVLKLAKGDEVWLRMGNGALHGDHQRFFSTFAGF 240  
QY 241 LLFETK 246  
Db 241 LLFETK 246  
RESULT 8  
ID AAM99925  
XX AAM99925 standard; Protein; 225 AA.  
AC AAM99925;  
XX

DT 07-JAN-2002 (first entry)  
XX Human polypeptide SEQ ID NO 41.  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
XX vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.  
XX Homo sapiens.  
XX WO200155173-A2.  
XX 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01356.  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-020515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 14-JUL-2000; 2000US-0217496.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 12-SEP-2000; 2000US-0232081.  
PR 14-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.



PR 14-SEP-2000; 2000US-0232400.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235836.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 13-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249246.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI WPI; 2001-451924/48.  
 XX N-PSDB; AA199523.  
 DR New nucleic acids and polypeptides, useful for treating, preventing or  
 PT ameliorating human disorders and diseases -  
 PT Claim 11; SEQ ID NO 41; 465pp + Sequence Listing; English.  
 XX The invention relates to novel human polynucleotides (AA199513-AA199538)  
 CC and the encoded proteins (AAM99915-AAM99934) which are useful for  
 CC preventing, treating or ameliorating medical conditions e.g. by protein  
 CC or gene therapy. The genes are isolated from a range of human tissues  
 CC disclosed in the specification. The nucleic acids, proteins, antibodies  
 CC and (ant)agonists are useful in the diagnosis, treatment and prevention  
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemia; (d) wound healing; and (e) neurological diseases  
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as  
 CC viral, bacterial, fungal and parasitic infections.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 225 AA;  
 Query Match 88.4%; Score 1208; DB 22; Length 225;  
 Best Local Similarity 99.5%; Pred. No. 4.9e-109;  
 Matches 218; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 28 ESPQTGGLPPDCCKCHGYSFRGYQGGPPGPPGIPGNHGNNGNNGATGCAKGEKG 87  
 Db 7 QSPQTGGLPPDCCKCHGYSFRGYQGGPPGPPGIPGNHGNNGNNGATGCAKGEKG 66  
 Qy 88 DKGDLGPRGERGQHGPKGKGYPGIPPELQIAFASLATHFSNQNIGFVSFVETNIGNF 147  
 Db 67 DKGDLGPRGERGQHGPKGKGYPGIPPELQIAFASLATHFSNQNIGFVSFVETNIGNF 126  
 Qy 148 FDMVTGREGAPVSGVYFFTFSSMKHEDVEEYVYLHNGNTVFSMYEMKGSQDTSNNH 207  
 Db 127 FDMVTGREGAPVSGVYFFTFSSMKHEDVEEYVYLHNGNTVFSMYEMKGSQDTSNNH 186  
 Qy 208 AVLKLAKGDEVWLRMGNGALHGDHQRFTFAGFLLFETK 246  
 Db 187 AVLKLAKGDEVWLRMGNGALHGDHQRFTFAGFLLFETK 225  
 RESULT 9  
 AAM41860  
 ID AAM41860 standard; Protein: 202 AA.  
 XX  
 AC AAM41860;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX Human polypeptide SEQ ID NO 6791.  
 XX

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS Homo sapiens.  
 XX WO200153312-A1.  
 XX PD 26-JUL-2001.  
 XX PF 26-DEC-2000; 2000WO-US34263.  
 XX PR 21-JAN-2000; 2000US-0488725.  
 XX PR 25-APR-2000; 2000US-052317.  
 XX PR 09-JUL-2000; 2000US-0598042.  
 XX PR 19-JUL-2000; 2000US-0620312.  
 XX PR 03-AUG-2000; 2000US-0653450.  
 XX PR 14-SEP-2000; 2000US-0662191.  
 XX PR 19-OCT-2000; 2000US-0693036.  
 XX PR 29-NOV-2000; 2000US-0727344.  
 XX (HYSE-) HYSEQ INC.  
 XX PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX XX  
 XX WPI: 2001-442253/47.  
 XX DR N-PSDB; AAI61016.  
 XX XX  
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders  
 XX PT such as central nervous system injuries -  
 XX XX  
 XX PS Example 2; SEQ ID NO 6791; 10078pp; English.  
 XX XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 202 AA;  
 Query Match 64.7%; Score 884; DB 22; Length 202;  
 Best Local Similarity 84.2%; Pred. No. 1.2e-77;  
 Matches 170; Conservative 0; Mismatches 0; Indels 32; Gaps 1;  
 QY 77 TGEGAGKEGKGDLDGPRGEGHCPGKGYGPIPE----- 115  
 Db 1 TGEGAGKEGKGDLDGPRGEGHCPGKGYGPIPELPGWSAVVSWLTAATKKVQA 60  
 QY 116 -----LQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMTRGFCAPVSGVYF 164  
 Db 61 ILLPOPLEXLGLQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMTRGFCAPVSGVYF 120  
 QY 165 FTFSMMKHEDVEEYVYLLMHNGNTVFSYEMKGSKDTSSNHAHLKAKGDVWLRMGN 224  
 Db 121 FTFSMMKHEDVEEYVYLLMHNGNTVFSYEMKGSKDTSSNHAHLKAKGDVWLRMGN 180

QY 225 GALHGDHQRFSFAGFLLETK 246  
 Db 181 GALHGDHQRFSFAGFLLETK 202  
 RESULT 10  
 AAE06589  
 ID AAE06589 standard; Protein; 223 AA.  
 XX AC AAE06589;  
 XX DT 25-SEP-2001 (first entry)  
 XX DE Human protein having hydrophobic domain, HP10781.  
 XX KW Human; hydrophobic domain; gene therapy; nutritional supplement;  
 KW cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial;  
 KW multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes;  
 KW haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic;  
 KW Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic;  
 KW haemostatic; thrombolytic; tumour growth inhibitor; anabolic;  
 KW contraceptive; antiinfertility; antiinflammatory.  
 XX OS Homo sapiens.  
 XX PN WO200149728-A2.  
 XX PD 12-JUL-2001.  
 XX PF 28-DEC-2000; 2000WO-JP09359.  
 XX PR 06-JAN-2000; 2000JP-0000585.  
 XX PR 06-JAN-2000; 2000JP-0000588.  
 XX PR 11-JAN-2000; 2000JP-0002299.  
 XX PR 03-FEB-2000; 2000JP-0026862.  
 XX PR 03-MAR-2000; 2000JP-0058367.  
 XX PA (PROT-) PROTEGENE INC.  
 XX PI (SAGA) SAGAMI CHEM RES CENT.  
 XX PI Kato S, Kimura T;  
 XX WPI: 2001-418355/44.  
 XX DR N-PSDB; AAD12584.  
 XX PT Human proteins with hydrophobic domains and the nucleic acids encoding  
 XX them, useful for preventing diagnosing and treating e.g. cancer,  
 XX Alzheimer's and inflammation -  
 PS Claim 1; Page 308-309; 563pp; English.  
 CC The present sequence is human protein with hydrophobic domain,  
 CC HP10781. The polynucleotide and polypeptide of the invention  
 CC may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The polynucleotides  
 CC may be used to produce the polypeptide, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the protein. The  
 CC polynucleotides and its complementary sequences may also be used as DNA  
 CC probes in diagnostic assays and also used in gene therapy. The  
 CC polypeptides may also be used as antigens in the production of antibodies  
 CC and in assays to identify modulators of polypeptide expression and  
 CC activity. The polypeptides and nucleic acids may be used as nutritional  
 CC supplements, to modulate cytokine and cell proliferation activity, to  
 CC modulate immune stimulation or suppression (e.g. for the treatment of  
 CC microbial infections and autoimmune disorders such as multiple sclerosis,  
 CC rheumatoid arthritis and insulin-dependent diabetes), to modulate  
 CC haematopoiesis, to modulate tissue growth activity (e.g. for the  
 CC treatment of Parkinson's disease, Huntington's disease and Alzheimer's  
 CC disease), to modulate activin and inhibin activity (e.g. for controlling  
 CC fertility), to modulate chemotactic and chemokinetic activity, to  
 CC modulate haemostatic and thrombolytic activity, to modulate receptor  
 CC ligand activity, to modulate inflammation and to inhibit tumour growth.  
 XX

SQ Sequence 223 AA;  
Query Match 58.08; Score 792.5; DB 22; Length 223;  
Best Local Similarity 66.86; Pred. No. 1e-68;  
Matches 147; Conservative 0; Mismatches 0; Indels 73; Gaps 1;  
QY 1 MLWRQLIYWQLLALFFLPFCCLQDEYME-----SPQTGGLPPDCSKCCHGDY 28  
DB 1 MLWRQLIYWQLLALFFLPFCCLQDEYMEVSGRTNKVARIYVQSHQQTGRSGSRREKVRER 60  
QY 29 -----SPQTGGLPPDCSKCCHGDY 47  
DB 61 SHPKTGTVDNNTSLKSLRDELPHPEVDLQITTFWGSQPTGGLPPDCSKCCHGDY 120  
QY 48 SFRGYQGGPPGPPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGK 107  
DB 121 SFRGYQGGPPGPPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGK 180  
QY 108 GYPGIPPELQIAFASLASLATHESNONGIIFSVETNIGNF 147  
DB 181 GYPGIPPELQIAFASLASLATHESNONGIIFSVETNIGNF 220  
RESULT 11  
AAY11485  
ID AAY11485 standard; Protein: 128 AA.  
XX AC AAY11485;  
XX DT 21-JUN-1999 (first entry)  
XX DE Human 5' EST secreted protein SEQ ID NO 307.  
XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis;  
XX KW forensic; gene therapy; chromosome mapping; signal peptide;  
XX KW upstream regulatory sequence; cytokine activity; cell proliferation;  
XX KW differentiation; haematopoiesis regulation; tissue growth regulation;  
XX KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;  
XX KW thrombolytic; anti-inflammatory; tumour inhibition.  
XX OS Homo sapiens.  
XX PN WO9906551-A2.  
XX PD 11-FEB-1999.  
XX PF 31-JUL-1998; 98WO-IB01235.  
XX PR 01-AUG-1997; 97US-0905133.  
XX PA (GEST ) GENSET.  
XX PI Duclert A, Dumas Milne Edwards J, Lacroix B;  
XX DR WPI; 1999-153781/13.  
XX DR N-PSDB; AAX39551.  
XX PT New nucleic acids encoding human secreted - proteins obtained from  
PT cDNA libraries prepared from substantia nigra, cerebellum, surrenals  
PT and fetal brain tissue  
XX PS Claim 34; Page 402-403; 434pp; English.  
XX CC AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for  
CC human secreted proteins, and encode the proteins given in AAY11374 to  
CC AAY11531, respectively. The proteins given represent the signal peptide  
CC and an N-terminal fragment of a secreted protein. The nucleic acid  
CC sequences can be used for producing secreted human gene products. The  
CC can also be used to develop products for diagnosis and therapy. The  
CC proteins obtained may have cytokine activity, cell  
CC proliferation/differentiation activity, haematopoiesis regulating  
CC activity, tissue growth regulating activity, reproductive hormone  
CC regulating activity, chemotactic/ chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ ligand activity, anti-inflammatory  
CC activity, tumour inhibition activity or other activities. The products  
CC can be used in forensic, gene therapy and chromosome mapping procedures.  
CC The sequences can also be used for obtaining corresponding promoter  
CC sequences. The nucleic acids encoding the signal peptide can be used for  
CC directing extracellular secretion of a polypeptide or the insertion of a  
CC polypeptide into a membrane, or importing a polypeptide into a cell.  
XX SQ Sequence 128 AA;  
Query Match 52.7%; Score 721; DB 20; Length 128;  
Best Local Similarity 100.0%; Pred. No. 4.2e-62;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLWRQLIYWQLLALFFLPFCCLQDEYMESPTGGLPPDCSKCCHGDYSFRGYQGGPPG 60  
DB 1 MLWRQLIYWQLLALFFLPFCCLQDEYMESPTGGLPPDCSKCCHGDYSFRGYQGGPPG 60  
QY 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGIPPELQIAF 120  
DB 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKGYGIPPELQIAF 120  
QY 121 MASL 124  
DB 121 MASL 124  
RESULT 12  
AAM40074  
ID AAM40074 standard; Protein: 126 AA.  
XX AC AAM40074;  
XX DT 22-OCT-2001 (first entry)  
XX DE Human polypeptide SEQ ID NO 3219.  
XX KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX OS Homo sapiens.  
XX PN WO200153312-A1.  
XX PD 26-JUL-2001.  
XX PF 26-DEC-2000; 2000WO-US34263.  
XX PR 21-JAN-2000; 2000US-0488725.  
XX PR 25-APR-2000; 2000US-0552317.  
XX PR 09-JUL-2000; 2000US-0598042.  
XX PR 19-JUL-2000; 2000US-0620312.  
XX PR 03-AUG-2000; 2000US-0653450.  
XX PR 14-SEP-2000; 2000US-0662191.  
XX PR 19-OCT-2000; 2000US-0693036.  
XX PR 29-NOV-2000; 2000US-0727344.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao Qa, Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
XX DR N-PSDB; AAI59230.  
XX PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -

Example 5; SEQ ID NO 3219; 10078pp; English.

PS The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 XX the encoded polypeptides (AAI38642-AAI42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-brager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX SQ Sequence 126 AA;

Query Match 48.5%; Score 663; DB 22; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-56;  
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 MASLATHFSNQSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFFSMMKHEDVEEYV 180  
 DB 1 MASLATHFSNQSGIIFSSVETNIGNFDVMTGRFGAPVSGVYFFFSMMKHEDVEEYV 60  
 QY 181 YLMHNGNTVFSMYEMKGSQDSSNHAUJLAKGDEWLRMGALHGDRFSTFAGF 240  
 DB 61 YLMHNGNTVFSMYEMKGSQDSSNHAUJLAKGDEWLRMGALHGDRFSTFAGF 120  
 QY 241 LLFETK 246  
 DB 121 LLFETK 126

RESULT 13

AAV75969  
 ID AAV75969 standard; Protein; 105 AA.

XX AC AAV75969;

XX DT 27-MAR-2000 (first entry)

XX DE Rat skin cell protein, SEQ ID 147.

XX KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
 KW secreted; transmembrane; inflammation; cancer; neurological disease;  
 KW angiogenesis; tumour vascularisation; growth disorder;  
 KW developmental disorder; skin wound; hair follicle disorder;  
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX OS Rattus sp.

XX PN WO9955865-A1.

XX PD 04-NOV-1999.

XX PF 29-APR-1999; 99WO-NZ00051.

XX PR 29-APR-1998; 98US-0069726.

XX PR 09-NOV-1998; 98US-0188930.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;  
 XX WPI; 2000-072177/06.

XX Novel polynucleotides useful for the treatment of various conditions

PT including wounds and cancer -

XX Claim 4; Page 112-113; 235pp; English.

XX CC The invention relates to novel nucleic acid sequences derived from rat  
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
 CC cells. Polypeptides of the invention may be used to treat inflammation,  
 CC cancer and neurological diseases. The proteins may be used to stimulate  
 CC the growth and motility of keratinocytes, to inhibit the growth of  
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
 CC modulate skin inflammation, to modulate epithelial cell growth and to  
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
 CC to treat growth and developmental defects, skin wounds and hair follicle  
 CC disorders. Sequences AAV75942-Y76123 represent polypeptides encoded  
 CC by cDNA sequences derived from several mouse, rat or human skin cell  
 CC types. Sequences AAV75942-Y75947, AAV76020-Y76021, AAV76094-Y76104 and  
 CC AAV76119 are proteins with an N-terminal signal sequence, indicating  
 CC that they are secreted. Sequences AAV75986-Y75989, AAV76061-Y76071,  
 CC AAV76106-Y76109 and AAV76121-Y76122 are proteins with one or more  
 CC putative transmembrane domains.

XX SQ Sequence 105 AA;

Query Match 42.6%; Score 582; DB 21; Length 105;  
 Best Local Similarity 93.3%; Pred. No. 1e-48;  
 Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLIYWOLLALFLPFCLODEYMESQGTGLPPDCSKCHGYSFRGYGPPGPPG 60

DB 1 MLRRQLVWHLALLFLPFCLODEYMESQAGGLPPDCSKCHGYSFRGYGPPGPPG 60

QY 61 PCGIPGNHGNNGNNGATGHEGAKGEKGDGLGPRGQHGPKG 105

DB 61 PCGIPGNHGNNGNNGATGHEGAKGEKGDGLGPRGQHGPKG 105

RESULT 14

AAV76025  
 ID AAV76025 standard; Protein; 105 AA.

XX AC AAV76025;

XX DT 27-MAR-2000 (first entry)

XX DE Rat skin cell protein, SEQ ID NO:280.

XX KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
 KW secreted; transmembrane; inflammation; cancer; neurological disease;  
 KW angiogenesis; tumour vascularisation; growth disorder;  
 KW developmental disorder; skin wound; hair follicle disorder;  
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX OS Rattus sp.

XX PN WO9955865-A1.

XX PD 04-NOV-1999.

XX PF 29-APR-1999; 99WO-NZ00051.

XX PR 29-APR-1998; 98US-0069726.

XX PR 09-NOV-1998; 98US-0188930.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;  
 XX WPI; 2000-072177/06.

XX DR N-PSDB; AAZ61730.

XX Novel polynucleotides useful for the treatment of various conditions

PT including wounds and cancer -

PS Claim 4; Page 168; 235pp; English.

XX The invention relates to novel nucleic acid sequences derived from rat  
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
 CC cells. Polypeptides of the invention may be used to treat inflammation,  
 CC cancer and neurological diseases. The proteins may be used to stimulate  
 CC the growth and motility of keratinocytes, to inhibit the growth of  
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to  
 CC modulate skin inflammation, to modulate epithelial cell growth and to  
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used  
 CC to treat growth and developmental defects, skin wounds and hair follicle  
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded  
 CC by cDNA sequences derived from several mouse, rat or human skin cell  
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and  
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating  
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,  
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more  
 CC putative transmembrane domains.

XX Sequence 105 AA;

Query Match 42.6%; Score 582; DB 21; Length 105;

Best Local Similarity 93.3%; Pred. No. 1e-48;

Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 MLWRQLIYWQLLALLFLPFCCLQDEYMESPTQGGIPLPPDCSKCHGDYSGRGYQGGPPPG 60

DB 1 MLRRQLVVMHLLALLFLPFCCLQDEYMESPTQAGGLPPDCSKCHGDYSGRGYQGGPPPG 60

OY 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

DB 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

RESULT 15

AAB55908

ID AAB55908 standard; Protein; 105 AA.

XX AAB55908;

AC AAB55908;

DT 08-MAR-2001 (first entry)

DE Skin cell protein, SEQ ID NO: 147.

XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;  
 KW neutropic; neuroprotective; vulnary; immunomodulatory; vaccine;  
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;  
 KW inflammation; neurological disease.

OS Rattus sp.

XX WO200069884-A2.

PN 23-NOV-2000.

XX 15-MAY-2000; 2000WO-NZ00075.

XX 14-MAY-1999; 99US-0312283.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR WPI; 2001-007495/01.

XX N-PSDB; AAC99566, AAC99776.

XX New isolated polynucleotide used in the identification of genetic  
 PT disorders and encoding polypeptides used for treating inflammatory  
 PT disease, cancer and neurological diseases -

XX

PS Claim 4; Page 147; 352pp; English.

XX The present sequence is a polypeptide which is expressed in  
 CC mammalian skin cells. The polypeptide is useful for stimulating  
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,  
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
 CC tumours, modulating skin inflammation, stimulating the growth of  
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus  
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
 CC neurological diseases. The polynucleotide can be used as a marker, in  
 CC the identification of genetic disorders, and for the design of  
 CC oligonucleotides for examining expression patterns.

SQ Sequence 105 AA;

Query Match 42.6%; Score 582; DB 22; Length 105;

Best Local Similarity 93.3%; Pred. No. 1e-48;

Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 MLWRQLIYWQLLALLFLPFCCLQDEYMESPTQGGIPLPPDCSKCHGDYSGRGYQGGPPPG 60

DB 1 MLRRQLVVMHLLALLFLPFCCLQDEYMESPTQAGGLPPDCSKCHGDYSGRGYQGGPPPG 60

OY 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

DB 61 PPGIPGNHNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKG 105

Search completed: January 13, 2003, 10:42:49

Job time : 38 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:48 ; Search time 15 Seconds  
(without alignments)  
482.536 Million cell updates/sec

Title: US-09-931-836-2  
Perfect score: 1367  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pap.\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pap.\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pap.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pap.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	42.6	105	US-09-188-930-147	Sequence 147, App
2	582	42.6	105	US-09-188-930-280	Sequence 280, App
3	316	23.1	294	US-09-188-930-294	Sequence 294, App
4	294	21.5	247	US-08-463-911-2	Sequence 2, Appl
5	293.5	21.5	231	US-09-530-423-2	Sequence 2, Appl
6	293.5	21.5	244	US-08-463-911-7	Sequence 7, Appl
7	293.5	21.5	244	US-09-140-804-3	Sequence 3, Appl
8	293.5	21.5	244	US-09-336-536-20	Sequence 20, Appl
9	287	21.0	247	US-09-530-423-1	Sequence 1, Appl
10	287	21.0	247	US-09-140-804-8	Sequence 8, Appl
11	287	21.0	247	US-09-118-408-3	Sequence 3, Appl
12	287	21.0	247	US-09-506-855-3	Sequence 3, Appl
13	274	20.0	246	US-08-463-911-4	Sequence 4, Appl
14	273	20.0	746	US-09-370-838-185	Sequence 185, App
15	264.5	19.3	228	US-09-336-536-4	Sequence 4, Appl
16	264.5	19.3	243	US-09-140-804-2	Sequence 2, Appl
17	264.5	19.3	243	US-09-336-536-3	Sequence 3, Appl
18	254.5	18.6	243	US-09-336-536-10	Sequence 10, Appl
19	252.5	18.5	228	US-09-336-536-11	Sequence 11, Appl
20	252.5	18.5	243	US-09-188-930-295	Sequence 295, App
21	237.5	17.4	281	US-09-118-408-44	Sequence 44, Appl
22	237.5	17.4	281	US-09-506-855-44	Sequence 44, Appl
23	226	16.5	281	US-09-118-408-2	Sequence 2, Appl
24	226	16.5	281	US-09-506-855-2	Sequence 2, Appl
25	226	16.5	423	US-08-383-744-2	Sequence 2, Appl
26	226	16.5	423	US-08-999-336-2	Sequence 2, Appl
27	226	16.5	423	PCT-US96-01427-2	Sequence 2, Appl

28	219	16.0	245	4	US-09-140-804-4	Sequence 4, Appl
29	202	14.8	215	4	US-09-140-804-5	Sequence 5, Appl
30	200.5	14.7	198	4	US-09-188-930-138	Sequence 138, App
31	196	14.3	222	4	US-09-140-804-7	Sequence 7, Appl
32	194	14.2	185	2	US-08-463-911-3	Sequence 3, Appl
33	192	14.0	623	4	US-09-029-348-3	Sequence 3, Appl
34	192	14.0	626	4	US-09-029-348-2	Sequence 2, Appl
35	186	13.6	236	4	US-09-140-804-6	Sequence 6, Appl
36	185	13.5	357	1	US-07-609-716-66	Sequence 66, Appl
37	185	13.5	357	1	US-08-642-255-33	Sequence 33, Appl
38	185	13.5	357	4	US-08-475-411A-66	Sequence 66, Appl
39	185	13.5	357	4	US-08-478-029A-66	Sequence 66, Appl
40	184.5	13.5	684	1	US-08-555-669-12	Sequence 12, Appl
41	184.5	13.5	684	3	US-09-073-663-12	Sequence 12, Appl
42	183.5	13.4	532	1	US-08-494-168-9	Sequence 9, Appl
43	183	13.4	489	2	US-08-794-795-7	Sequence 7, Appl
44	183	13.4	489	4	US-09-249-200-7	Sequence 7, Appl
45	183	13.4	518	1	US-08-392-367B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-188-930-147  
; Sequence 147, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murlison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 147  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-188-930-147  
Query Match 42.6%; Score 582; DB 4; Length 105;  
Best Local Similarity 93.3%; Pred. No. 2.1e-51;  
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 MLWRLIYWQLLALFLPFCLODEYMEPOTGGLPDCKCKCHGDSYFRGYQGPPGPG 60  
Db 1 MLRRLVWHLALLFLPFCLODEYMEPQAGGLPPDCKCKCHGDSYFRGYQGPPGPG 60  
Qy 61 PPGIFGNHNNNGATGHEGAKGDKGDKGLGPRGERGQHGPKG 105  
Db 61 PPGIFGNHNNNGATGHEGAKGDKGDKGLGPRGERGQHGPKG 105  
RESULT 2  
US-09-188-930-280  
; Sequence 280, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murlison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; TITLE OF INVENTION: and Methods For Their Use  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 280  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-188-930-280

Query Match 42.6%; Score 582; DB 4; Length 105;  
Best Local Similarity 93.3%; Pred. No. 2.1e-51;  
Matches 98; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MLWRQLIYWOLLALFLPCLCQDEYMESPTGGLPPDCSKCHGYSFRGYQGPPGPPG 60

Db 1 MLRRQLVWHLALLFLPCLCQDEYMESPAAGLPPDCSKCHGDFGRGYQGPPGPPG 60

QY 61 PPGIPGNHGNNGNNGATGHEGAKGKGDGLGPRGERGQHPKG 105

Db 61 PPGIPGNHGNNGNNGATGHEGAKGKGDGLGPRGERGQHPKG 105

## RESULT 3

US-09-188-930-294  
; Sequence 294, Application US/09188930A  
; Patent No. 6150502

; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Mathew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

; TITLE OF INVENTION: Compositions Isolated From Skin Cells

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 294

; LENGTH: 294

; TYPE: PRT

; ORGANISM: Rat

US-09-188-930-294

Query Match 23.1%; Score 316; DB 4; Length 294;

Best Local Similarity 28.9%; Pred. No. 5.7e-24;

Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;

QY 6 LIYWQLIALFLPCLCQDEYM-----ESPQTGGLPPDCSKCHGYSFRGYQGPPGPP 59

Db 10 MISWMLLAC-ALP--CAADPMLGAFARRDFQKGPQLVCS-----LPGQGP 54

QY 60 GPPGIPGNHGNNGNNGATGHEGAKGKGD-----L 92

Db 55 GPPGAPGSSGMVGMFPKGDQGDGRDSDGEGPGRTGNRGKQPKKAGAI 114

QY 93 GPRGER-----COHGPKEGYPGIP-----PELQIAFMASLATHFSNQNS 133

Db 115 GPRGPGVSTPKHGIPKKGKGRKSAFSAVTKSYPRERL 174

QY 134 GIIFSSVETNIGNFFDMVTRFCGAPYSGVYFFTFNM-----KHEDVEVYVYLMHNGNTVF 190

Db 175 PIFDKILMNEGHYANSSGKFCVSPGIYFYDTITLANKH-----LAIGLVHNGQ--Y 227

QY 191 SMYSYEMK-GKSDTSSNHAVLKIAKDEVLWM-----GNGALHGDHQRSTFAGFLF 243

Db 228 RIRTFDANTGNHDVAGSSTILALKEGDEVWLQIFYSEQNGFLFYDPYWTDSLTGFLIY 285

## RESULT 4

US-08-463-911-2

; Sequence 2, Application US/08463911

; Patent No. 5869330  
; GENERAL INFORMATION:  
; APPLICANT: Scherer, Philipp E.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,911

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WHI95-05

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-463-911-2

Query Match 21.5%; Score 294; DB 2; Length 247;

Best Local Similarity 31.5%; Pred. No. 7.4e-22;

Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

QY 6 LIYWQLIALFLPCLCQDEYMESPTGG--LPPDCSKCHGYSFRGYQGPPGPPG 63

Db 2 LLLQALLFLLLP-SHAEDDVTTTEELAPALVPPKGTCA-----GMA--GIPG 48

QY 64 IPGNHGNNGNNGATGHEGAKGKGDGLGPRGER---GOHGPKEGYPGIPPE----- 115

Db 49 HPNGHTPGDRDGTGPEKGEKGDAGLLGPKGETGDVGMTGAEGRPGFTGPRKGE 108

QY 116 ----LQIAFMASLATHFSNQNSGIIFSSVETNIGNFFDMVTRFCGAPYSGVYFFTF 170

Db 109 EAYMTRSAPSVGLETRVTPNVPPIRFTKIFYNQNHYDGTGKFCYNIGLIFYFSHIT 168

QY 171 KHEDVEVYVYLMHNGNTVFSMYSYEMKSDTSSNHAVLKIAKDEVLWM--GNG--A 226

Db 169 VY--MKDVKYSLFKKDAVLFTYDQYQEKNVDAQSGVLLHLEVGQVQLQVYGDG 226

QY 227 LHGDHQRSTFAGFLF 243

Db 227 LYADNVNDSTFTGFLY 243

## RESULT 5

US-09-530-423-2

; Sequence 2, Application US/09530423

; Patent No. 6461821

; GENERAL INFORMATION:

; APPLICANT: Otsuka Pharmaceutical Co., Ltd.

; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a

; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit

; TITLE OF INVENTION: therefor

; FILE REFERENCE: P98-51



```

Query Match          21.5%; Score 293.5; DB 2; Length 244;
Best Local Similarity 34.5%; Pred No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps

Qy 53 QGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGEKDKG---LGPR---GE 97
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPEKGEKGDPLGPKGDIGE 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 98 RQGHGPKGEKYPGI-----PPE-----LQIAFMASLATHFSNQNSGIIFFSSVETNIGNF 147
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKKGPGEGAYVYRSAFSVGLTFTVTPNMPIRFTKIFYNQNH 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 148 FDMVTGRGAPVSGVYPTFETSMKMHDEVEVYVYLMHNGNTVFESMYSYEMKGSDDTSSNH 200
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGFHCNIPGLYFAHIIVY--MKDKVLSLFFKKDKAMLFTTYDQYQENNVDAQSGS 200
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 208 AVLKLAKGDEWLRM-GNG---ALHGDHQRFEFTFAGFLF 243
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLY 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US-09-140-804-3
; Sequence 3, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-140-804-3

Query Match          21.5%; Score 293.5; DB 4; Length 244;
Best Local Similarity 34.5%; Pred. No. 8.2e-22;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps

Qy 53 QGP-----PGPPG-----PGIPGNHNGNNGATGHEGAKGEKDKG---LGPR---GE 97
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 QGPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTPEKGEKGDPLGPKGDIGE 82
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 98 RQGHGPKGEKYPGI-----PPE-----LQIAFMASLATHFSNQNSGIIFFSSVETNIGNF 147
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TGVPGAEGPRGPGIQRKKGPGEGAYVYRSAFSVGLTFTVTPNMPIRFTKIFYNQNH 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 148 FDMVTGRGAPVSGVYPTFETSMKMHDEVEVYVYLMHNGNTVFESMYSYEMKGSDDTSSNH 207
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 YDGTGFHCNIPGLYFAHIIVY--MKDKVLSLFFKKDKAMLFTTYDQYQENNVDAQSGS 200
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 208 AVLKLAKGDEWLRM-GNG---ALHGDHQRFEFTFAGFLF 243
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLY 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-336-536-20
; Sequence 20, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

```



Db 2 LLLQALLFLILP-SHAEDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48  
QY 64 IPGNHNGNNGATGHEGAKGKGDGLGPRGER--GQHPKGEKGYG-----GIPP 114  
Db 49 HPGHNGTPGRDGRDTPGKGEKGDAGLLGPKGETGDVMTGAEGPRGPQTGPKRGEPP 108  
QY 115 E----LQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMGRGAPVSGVYFFTFSMX 170  
Db 109 EAAWYRSFVSGLETRVTPVNPVIRTKIFYNQNHQHDGSGTKFCYNIPGLYFYSYHIT 168  
QY 171 KHEDEVEVYVYLMHNGNTVFSMYSEMKGKSDTSSNHAHLKAKGDEVWLRM-GNG---A 226  
Db 169 VY--MKDVKVSFLFKDKAVLFTYDQYQKENVQDQAGSVLLHLEVGQVWLQVYGDGDHNG 226  
QY 227 LHGDHORESTFAGFLLF 243  
Db 227 LYADNVNDSTFTGFLLY 243

RESULT 12  
US-09-506-835-3  
; Sequence 3, Application US/09506855  
; Patent No. 6448221  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; TITLE OF INVENTION: IMMUNE FUNCTION  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/09/506.855  
; CURRENT FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-506-855-3

Query Match 21.0%; Score 287; DB 4; Length 247;  
Best Local Similarity 31.9%; Pred. No. 3.8e-21;  
Matches 82; Conservative 40; Mismatches 101; Indels 34; Gaps 10;  
QY 6 LIYWOLLALFFLPCLCQDYMESPTGG--LPPDCSKCCHGDSYFRGYQGPFGPPGPPG 63  
Db 2 LLLQALLFLILP-SHAEDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48  
QY 64 IPGNHNGNNGATGHEGAKGKGDGLGPRGER--GQHPKGEKGYG-----GIPP 114  
Db 49 HPGHNGTPGRDGRDTPGKGEKGDAGLLGPKGETGDVMTGAEGPRGPQTGPKRGEPP 108  
QY 115 E----LQIAFMASLATHFSNQSGIIFSSVEINIGNFFDVMGRGAPVSGVYFFTFSMX 170  
Db 109 EAAWYRSFVSGLETRVTPVNPVIRTKIFYNQNHQHDGSGTKFCYNIPGLYFYSYHIT 168  
QY 171 KHEDEVEVYVYLMHNGNTVFSMYSEMKGKSDTSSNHAHLKAKGDEVWLRM-GNG---A 226  
Db 169 VY--MKDVKVSFLFKDKAVLFTYDQYQKENVQDQAGSVLLHLEVGQVWLQVYGDGDHNG 226  
QY 227 LHGDHORESTFAGFLLF 243  
Db 227 LYADNVNDSTFTGFLLY 243

RESULT 13  
US-08-463-911-4  
; Sequence 4, Application US/08463911  
; Patent No. 5869330  
; GENERAL INFORMATION:  
; APPLICANT: Scherer, Philipp E.  
; APPLICANT: Lodish, Harvey F.

; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
; TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/463.911  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granahan, Patricia  
; REGISTRATION NUMBER: 32,227  
; REFERENCE/DOCKET NUMBER: WHI95-05  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 246 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-463-911-4

Query Match 20.0%; Score 274; DB 2; Length 246;  
Best Local Similarity 31.3%; Pred. No. 7.6e-20;  
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;  
QY 51 GYGPPGPPGPPGIPGNHNGNNGATGHH-----EGAKGKGDGDLGPRGERGHPK 104  
Db 32 GYGIPGMPGMPGAPGKGDHGLGPKGEPGIPAVPTGPKGKGEPPGPHRGNGPR 91  
QY 105 GEKGYPIP-----PELQ-----IAFMASLATHFSNQSGIIFSSVETNIGNF 147  
Db 92 GTSGLPGDPPGPPGPPGPPGVEGRYKQKHSVETVTRQTYPEANALVRENSVVTNPQGH 151  
QY 148 FDMVTGRGAPVSGVYFFTFESMMKHEDVEEVYVLMHNGNTVFSM-----YSYEMK 198  
Db 152 YNPTGKFTCEVPLGYFVY-----YTSHANLCVHLNLNARVASFCDHMF 198  
QY 199 GKSDTSSNHAHLKAKGDEVWLRMG--NGALHGDHORESTFAGFLLF 243  
Db 199 NSKQVSSGALLRLQRGDEVWLSVNDYNGMV-GIEGNSNVFSGFLLF 244  
RESULT 14  
US-09-370-838-185  
; Sequence 185, Application US/09370838  
; Patent No. 6444425  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Mohamath, Roadoh  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF  
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE  
; FILE REFERENCE: 210121.475C1  
; CURRENT APPLICATION NUMBER: US/09/370.838  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: US 09/285,323  
; EARLIER FILING DATE: 1999-04-02  
; NUMBER OF SEQ ID NOS: 289

Search completed: January 13, 2003, 10:44:35  
Job time : 17 secs

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 185
; LENGTH: 746
; TYPE: prt
; ORGANISM: Homo sapien
US-09-370-838-185

```

Query Match 20.0%; Score 273; DB 4; Length 746;  
Best Local Similarity 29.6%; Pred. No. 4.4e-19;  
Matches 72; Conservative 43; Mismatches 90; Indels 38; Gaps 8;

34	GLPPDCSCCHGDYS-----FRGYOGPP-----	GP	CP	PG	PI	CG	NC	GN	GN	74
509	GLP-----SISNGNYSQLQFAREYSGAPI	SQ	RD	NF	QO	YK	KG	TS	GG	564
75	GATGHEGAKGKGDGLGPRGERQ-----	HG	PK	GE-----	KG	YP	GP	PI	PE	123
565	QVSSPE-RDNETFNSGDSQGDSSMT	PV	DV	PV	TN	PA	AT	IL	PV	622
124	LATHFS--NONGSILFSSVETNIGNEFF	DM	TC	RF	CA	PS	GV	YF	FT	181
623	RTSNLAPGTLDPFVFDLLNLNLGTFD	LQ	LG	RF	NC	PV	NG	T	V	682
182	LMHNGTVMFSYEMKGRKSDTSSN	HA	VL	KL	AK	GE	VM	LR	MG	241
683	LKNNEEVLVSAYNDGAPDHETASN	HA	IL	QL	FG	QI	WL	RL	HG	742
242	LFE 244									
743	LYQ 745									

```

RESULT 15
US-09-336-536-4
: Sequence 4, Application US/09336536
: Patent No. 6406984
: GENERAL INFORMATION:
: APPLICANT: Kely, K.
: APPLICANT: Mckay, C.
: APPLICANT: Bosstone, S.
: TITLE OF INVENTION: SECRETED PROTE
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 228
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-336-536-4

```

Query Match	19.3%	Score	264.5;	DB	4;	Length	228;
Best Local Similarity	32.4%	Ref. No.	6.3e-19;				
Matches	68;	Conservative	36;	Mismatches	79;	Indels	27;
						Gaps	7;

  

QY	56	GPQPQPGICPNHGN-----N	NNNGATGHEGAKGSKGD-----	KGDLGPRRGERGQ	100
dbb	14	PGHPLGLPTTGHGSGQGLPG	RDRDGRDGCAPAGPKGEGGR	PLGPRGDPGRGEAGP	73
QY	101	HGPKGKGYGPIPELQIAPMAS	LIATHFSNQNSGLITSSVE	NIINQNFDDVTMTGRGAPVS	160
dbb	74	AGPTGPAGECSVPPRSFA	SKRSERPPSPDAPLDFRVL	NEQGHYDVAVTGKFTQVPP	133
QY	161	GVYFETSMKHEDVEEYVY--	LMHNGNTVFSWYSYEMKG--	KDSTSSNAHVLLAKGD	216
dbb	134	GVYIFAV-----HATVYRAS	TFQLVKNGESIASFFQF--	FGGWPKASLGGGAVRLEPED	188
QY	217	EYWLRMNGN-----ALHGDH	QRFRSTFAGFLF	243	
dbb	189	OWWVOGVGDYIGIYASIK	TDSTFSGFLV	218	

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:03 ; Search time 19 Seconds  
(without alignments)  
1244.688 Million cell updates/sec

Title: US-09-931-836-2  
Perfect score: 1367  
Sequence: 1 MLWQLIYWQLLALFLPFC.....LHGDIHQRFSTFAGFLLETK 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293.5	21.5	244	JC4708	gelatin-binding 28
2	280.5	20.5	674	S3297	collagen alpha 1(X
3	278.5	20.4	680	S1216	collagen alpha 1(X
4	275	20.1	674	S13301	collagen alpha 1(X
5	274	20.0	246	S29328	complement subcomp
6	270	19.8	680	CGHUI0	collagen alpha 1(X
7	264.5	19.3	219	T14782	hypothetical prote
8	258.5	18.9	744	A34246	collagen alpha 1(V
9	255.5	18.8	744	S15435	collagen alpha 1(V
10	255	18.7	245	C1HUOC	complement subcomp
11	251.5	18.4	253	C1HUOB	complement subcomp
12	251.5	18.4	744	S23298	collagen alpha 1(V
13	249	18.2	635	A57131	collagen alpha 2(V
14	248	18.1	743	S23779	collagen alpha 1(V
15	239.5	17.5	245	S39018	complement subcomp
16	236.5	17.3	253	S49158	complement protein
17	231.5	16.9	253	S49560	complement Clq B c
18	226	16.5	423	A55797	collagen precursor
19	219	16.0	245	C1HUOA	complement subcomp
20	216	15.8	920	A45748	collagen alpha 1(V
21	215	15.7	992	T08772	collagen alpha 1(V
22	211.5	15.5	366	S11449	hypothetical prote
23	210.5	15.4	423	A41207	collagen short cha
24	208	15.2	2944	A54849	collagen 13, nonfi
25	207.5	15.2	775	A61228	collagen alpha 1(V
26	207.5	15.2	1549	A61228	collagen alpha 2(I
27	203.5	14.9	1707	A43526	type VII collagen
28	203.5	14.9	1712	CGHU28	collagen alpha 2(I
29	202	14.8	215	B48150	collagen alpha 2(I
					hibernation-relate

30 201 14.7 215 2 C48150 hibernation-relate  
31 197 14.4 171 2 A34493 collagen alpha 1(I  
32 196 14.3 224 2 A60032 cerabellin-like gl  
33 195.5 14.3 1315 2 A56101 collagen alpha 1(X  
34 195.5 14.3 1774 2 B56101 collagen alpha 1(X  
35 193.5 14.2 1744 2 S40991 collagen alpha 1(I  
36 193 14.1 296 2 A31219 collagen 1 - Caeno  
37 193 14.1 301 2 T21314 collagen alpha 1(I  
38 192.5 14.1 921 2 S42617 collagen alpha 1(I  
39 192 14.0 1466 1 CGHU7L collagen alpha 1(I  
40 190.5 13.9 289 2 T26812 collagen alpha 1(I  
41 189 13.8 193 2 A37873 collagen alpha 1(I  
42 189 13.8 375 1 A45225 collagen alpha 1(I  
43 189 13.8 1464 2 S59856 collagen alpha 1(I  
44 187.5 13.7 921 2 S40495 collagen alpha 1(I  
45 187 13.7 684 2 A53019 collagen alpha 1(X

ALIGNMENTS

RESULT 1

JC4708

gelatin-binding 28K protein precursor - human

N:Alternate names: adipose specific collagen-like factor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 20-Sep-1999

C:Accession: JC4708; JC4944

R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.

Biochem. Biophys. Res. Commun. 221, 286-289, 1996

A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor

A:Reference number: JC4708; MUID:96224171; PMID:8619847

A:Accession: JC4708

A:Molecule type: mRNA

A:Residues: 1-244 <MAE>

A:Cross-references: DBJ:D45371; NID:9871886; PID:BAA08227.1; PID:9871887

A:Experimental source: adipose tissue

R:Nakano, Y.; Tohe, T.; Choi-Miura, N.H.; Mazda, T.; Tomita, M.

J. Biochem. 120, 803-812, 1996

A:Title: Isolation and characterization of GBP28, a novel gelatin-binding protein pur

A:Reference number: JC4944; MUID:97103474; PMID:8947845

A:Accession: JC4944

A:Molecule type: protein

A:Residues: 19-38;93-100;101-112;135-149;173-178 <NAK>

C:Comment: This protein is an endogenous factor that binds with a collagen-like domai

C:Genetics:

A:Gene: apM1

C:Superfamily: unassigned collagens; complement Clq carboxyl-terminal homology

C:Keywords: adipose tissue; glycoprotein; hydroxyproline

F:1-18/Domain: signal sequence #status predicted <SIG>

F:19-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>

F:42-107/Region: collagen-like

F:114-241/Domain: complement Clq carboxyl-terminal homology <CIQ>

F:95/Modified site: 4-hydroxyproline (Pro) #status experimental

F:230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.5%; Score 293.5; DB 2; Length 244;

Best Local Similarity 34.5%; Pred. No. 7e-17;

Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

OY 53 OGP-----PCPPCP-----PGIPGNHGNNGNATGHEGAKGKGDGD---LGPR---GE 97

Db 23 OGPGLVLLPLKGACTGWNAGIPGPHNGAGPGRDGTTPGKGEKGDGLIGKDGIGE 82

OY 98 RQHGPKGKGYPGT-----PPE-----LQIAFMASLATHFSNQNSGIFFSVENIGNF 147

Db 83 TGVPCAEGPRGPGGLOGRKGEGEGAYVRSFVGLTYVTPNMPRTFTIFVYVNOQH 142

OY 148 FDMVTGRFCAPVSGVYFFTFSSMKHEDVEVYVYLMHNGNTVFSMYSYEMKSKSDTSNNH 207

Db 143 YDGSTGKFCNIPGLYFYFAYHITVY--MKDKVSLFKDKKAMLFYDQVQENNVQASGS 200

OY 208 AVLKLAKEGDEWLRM--GNG---ALHGDHQRFSTFAGFLLF 243



Db 503 EPLGPPGPPGPGQAVMPDGFIKAGQRPRLSGMPLVSANHGVTGMPVSAFTVILSKAY 562

Qy 129 SNQSGIIFSSVETNIGNFFDVMTRFGAPVSGVYFFTFSSMMKHEDVEEVVYLMHNGMT 188

Db 563 PAVGAPIPFDELINRQOHYDPRSGIFTCKIPGIYFYSYHV--HVKGTHVMVGLYKNGTP 620

Qy 189 VFSWYSYE--MKGSDTSSNNAVLKLAGDEVLWRMGN---GALHGDHQRSTFAGFL 242

Db 621 --TWTYDEYSKGYLDQAGSAIMELTENDQVWLQLPNAESNGLYSSEYVHSSFGFLV 677

## RESULT 4

S13301

collagen alpha 1(X) chain precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-Nov-1993 #sequence\_revision 23-Feb-1996 #text\_change 13-Aug-1999

C:Accession: S13301

R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.

Biochem. J. 273, 141-148, 1991

A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. Ev

A:Reference number: S13301; MUID:91113131; PMID:1703407

A:Accession: S13301

A:Molecule type: mRNA

A:Residues: 1-674 &lt;THO&gt;

A:Cross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264

C:Genetics:

A:Gene: COL10A1

C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology

C:Keywords: coiled coll; extracellular matrix; glycoprotein; homotrimer

F:1-18/Domain: signal sequence status predicted &lt;SIG&gt;

F:19-674/Product: collagen alpha 1(X) chain status predicted &lt;MAT&gt;

F:547-673/Domain: complement C1q carboxyl-terminal homology &lt;CIQ&gt;

Query Match

Best Local Similarity 20.1%; Score 275; DB 2; Length 674;

Matches 72; Conservative 31; Mismatches 87; Indels 50; Gaps 6;

Qy 51 GYQGPDPGPPGPGIPGNHNGNNGATGHEGAKGEKD-----KGDLPGRGERG 99

Db 434 GHNGEAGRGVPGIPGTRGPDPGPPGPGSGKGDVGTGPPGPAIAVKGLNGTPGPPG 493

Qy 100 QHGPKEKGVGPI-----PELQIA----FMASLATHFSNONSGII----- 136

Db 494 PPGPRNAGEPLGPPGPPGPGQVALPEDFVKAGQRFVSNQVGTGMPVSAFTVILS 553

Qy 137 -----FSSVETNIGNFFDVMTRFGAPVSGVYFFTFSSMMKHEDVEEVVYLMHN 185

Db 554 KAYPAIGTPIPFKILYNKQHYDPRGTGFTCKIPGIYFYSYHI--HVGKTHAWVGLYKN 611

Qy 186 GNTVFSMYSYEMKGSNTSSNNAVLKLAGDEVWLRM---GNCALHGDHQRSTFAGFL 242

Db 612 GTPVMYTYDEYIKGYLDQAGSVAIDLTDNDQVWLQLPNAGSNGLYSPEYVHSSFGFLV 671

RESULT 5

S29328

complement subcomponent C1q chain C - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Aug-1999

C:Accession: S29328

R:Petty, F.; Reid, K.B.M.; Loos, M.

Eur. J. Biochem. 209, 129-134, 1992

A:Title: Isolation, sequence analysis and characterization of cDNA clones coding for the

ecorebellin.

A:Reference number: S29328; MUID:93011118; PMID:1396691

A:Accession: S29328

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-246 &lt;PET&gt;

A:Cross-references: EMBL:X66295; NID:g50228; PIDN:CAA46993.1; PID:g50229

C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom

F:122-245/Domain: complement C1q carboxyl-terminal homology &lt;CIQ&gt;

Query Match 20.0%; Score 274; DB 2; Length 246;

Best Local Similarity 31.3%; Pred. No. 2.8e-15;

Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;

Qy 51 GYQGPDPGPPGPGIPGNHNGNNGATGHEGAKGEKGDGLDLPGRGERGQHGP 104

Db 32 GYGIPIGPGMPGAPGKGDHDLQGPKEGPIPAVPGTQGPQKGGKGEPMGHRGKNGPR 91

Qy 105 GEKYPGPI-----PELQ-----TAFMASLATHFSNONSGIIFSSVETNIGNF 147

Db 92 GTSGLPGDPGRPGPEGVGRYKQKHQSVFTVTRQTPYPEANALVRFSNVVTNPOGH 151

Qy 148 FDVMTGREGAPVSGVYFFTFSSMMKHEDVEEVVYLMHNGNTVESM-----YSYEMK 198

Db 152 YNPSTGKTCFVPGIYFYVY-----YTSHATANCLVHLNLNLARVASFCDHMF 198

Qy 199 GKSDTSSNNAVLKLAGDEVWLRM---NGALHGDHQRSTFAGFLF 243

Db 199 NSKVSSGGALLRLQGRDEVLSVNDYNGMV-GIEGSNSVFGFLF 244

RESULT 6

CCHUID

collagen alpha 1(X) chain precursor - human

N:Alternate names: procollagen alpha 1(X) chain

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 03-Nov-1995 #text\_change 22-Jun-1999

C:Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856

R:Reichenberger, E.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling,

FBES Lett. 311, 305-310, 1992

A:Title: Genomic organization and full-length cDNA sequence of human collagen X.

A:Reference number: S26396; MUID:93012005; PMID:1397333

A:Accession: S26396

A:Molecule type: DNA

A:Residues: 1-680 &lt;REI&gt;

A:Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB

R:Apte, S.S.

submitted to the EMBL Data Library, March 1992

A:Reference number: S30085

A:Accession: S30086

A:Molecule type: DNA

A:Residues: 'TTPFYGVWCVCLL', 52-680 &lt;APT&gt;

A:Cross-references: EMBL:X65120; NID:g23129

A:Note: the initial difference is probably due to translation of an intronic sequence

R:Apte, S.; Mattel, M.G.; Olsen, B.R.

FBES Lett. 282, 393-396, 1991

A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gen

A:Reference number: S15826; MUID:91243838; PMID:2037056

A:Accession: S15826

A:Molecule type: DNA

A:Residues: 561-647, 'G', 649-666 &lt;AP2&gt;

A:Cross-references: EMBL:X58879; NID:g30013; PIDN:CAA41686.1; PID:g30014

R:Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant

Biochem. J. 280, 617-623, 1991

A:Title: The human collagen X gene. Complete primary translated sequence and chromoso

A:Reference number: S18249; MUID:92109659; PMID:1764025

A:Accession: S18249

A:Molecule type: DNA

A:Residues: 1-26, 'T', 28-680 &lt;THO&gt;

A:Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095

A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-

R:Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.

Dev. Biol. 148, 562-572, 1991

A:Title: In situ hybridization studies on the expression of type X collagen in fetal

A:Reference number: A43901; MUID:92077285; PMID:1743401

A:Accession: A43901

A:Molecule type: mRNA

A:Residues: 547-656 &lt;RE2&gt;

A:Cross-references: GB:M74050; GB:D57494; NID:g339884; PIDN:AAA61221.1; PID:g553796

A:Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBI:P:69014)

R:Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant,

Am. J. Hum. Genet. 54, 169-178, 1994

A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal doma







	matches	/6;	Conservative	24;	Mismatches	104;	Indels	55;	Gaps	
QY	34	GLPPDCSKCHGNY	SFRGYQGPPGGPPIGNHGNNGNNGATCHEGA	-----KGE	85					

Qy	51	G Y O G P G P G P G I P O N H G N N G N G A T G - H E G A K G E K G D K G D ----- L G P	94
Db	31	K G D A G P N G R P C P G L K G E R G P G A A G I R T G I R G K D P G S G P G K P G N V G L P G P S G P	90
Qy	95	R G E R Q H G P K G E K Y P G - T P P E L Q I A F M A S L A T H F S N Q N S G I I F S V E T N I C N F D V W T G	153
Db	91	L G D S G P Q G L K V K G N P G N I R D Q P R P A F S A I R O N P M T L G N V - V I F O K V L T N O S P Y Q N H T G	149
Qy	154	R F C A P S V G Y I F F T S M M K H E D V E V Y V L M H N G -- N T V F S M K S Y E M W K G S D T S S H N H A V L K	211
Db	150	R F T C A P G V Y I F N F O V I S K W D L - C L F I K S S G Q P R D S L S F N T N N K G L F O V L A G T V L Q	208



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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:31:58 ; Search time 12 Seconds  
(without alignments)  
850.265 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367  
Sequence: 1 MLNRQLIYWQLLALFLPFC.....LHGDHQRFTFAGLLPFTK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1367	100.0	246	1 CQT3_HUMAN	Q9bxj4 homo sapien
2	315	23.0	289	1 COT7_HUMAN	Q9bx12 homo sapien
3	304	22.2	285	1 COT2_HUMAN	Q9bx15 homo sapien
4	297.5	21.8	258	1 C1RF_HUMAN	O75973 homo sapien
5	297.5	21.8	258	1 C1RF_MOUSE	O88992 mus musculus
6	294	21.5	247	1 APM1_MOUSE	Q60994 mus musculus
7	293.5	21.5	244	1 APM1_HUMAN	Q15848 homo sapien
8	289.5	21.2	278	1 COT6_HUMAN	Q9bx19 homo sapien
9	285.5	20.9	255	1 GLIC_MOUSE	O9esn4 mus musculus
10	280.5	20.5	674	1 CALA_CHICK	P08125 gallus gall
11	278.5	20.4	680	1 CALA_MOUSE	Q05306 mus musculus
12	275	20.1	674	1 CALA_BOVIN	P23206 bos taurus
13	274	20.0	246	1 C1QC_MOUSE	Q02105 mus musculus
14	270	19.8	680	1 CALA_HUMAN	Q03692 homo sapien
15	264.5	19.3	243	1 COT5_HUMAN	Q9bx10 homo sapien
16	258.5	18.9	744	1 COT5_RABIT	P14282 onychotagus
17	257.5	18.8	744	1 CAL8_HUMAN	P27658 homo sapien
18	257	18.8	743	1 CAL8_MOUSE	Q00780 mus musculus
19	255	18.7	245	1 C1QB_HUMAN	P02747 homo sapien
20	254	18.6	419	1 COLE_LEPMA	P98085 leptomys mac
21	251.5	18.4	251	1 C1QB_HUMAN	P02745 homo sapien
22	249	18.2	635	1 CA28_HUMAN	P25067 homo sapien
23	239.5	17.5	245	1 C1QA_MOUSE	P98086 mus musculus
24	236.5	17.3	253	1 C1QB_RAT	P31721 rattus norv
25	231.5	16.9	253	1 C1QB_MOUSE	P14106 mus musculus
26	226	16.5	281	1 COT1_HUMAN	Q9bxj1 homo sapien
27	219	16.0	245	1 C1QA_HUMAN	P02745 homo sapien
28	211.5	15.5	366	1 CAS4_EPHMU	P16503 ephydratia m
29	208	15.2	2944	1 CAL7_HUMAN	Q02388 homo sapien
30	203.5	14.9	1707	1 CA24_MOUSE	P08122 mus musculus
31	203.5	14.9	1712	1 CA24_HUMAN	P08572 homo sapien
32	202	14.8	215	1 HP25_TAMSI	Q06576 tamias sibi
33	201	14.7	215	1 HP27_TAMSI	Q06577 tamias sibi

34	200	14.6	1516	1 CALH_HUMAN	P39060 homo sapien
35	196	14.3	224	1 CERL_RAT	P98087 rattus norv
36	195.5	14.3	1527	1 CALH_MOUSE	P98061 mus musculus
37	195	14.3	458	1 COLQ_RAT	O35167 rattus norv
38	193.5	14.2	1758	1 CAL4_CAEEL	P17139 caenorhabdi
39	193	14.1	296	1 CC01_CAEEL	P08124 caenorhabdi
40	193	14.1	456	1 COLQ_HUMAN	Q97215 homo sapien
41	192	14.0	1466	1 CAL3_HUMAN	P03461 homo sapien
42	189	13.8	193	1 CERB_HUMAN	P23435 homo sapien
43	189	13.8	193	1 CERB_MOUSE	Q9r171 mus musculus
44	189	13.8	375	1 PSPD_HUMAN	P35247 homo sapien
45	189	13.8	1464	1 CAL3_MOUSE	P08121 mus musculus

#### ALIGNMENTS

RESULT 1  
CQT3\_HUMAN  
ID CQT3\_HUMAN STANDARD: PRT: 246 AA.  
AC Q9BXJ4; Q96KY1;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement-clq tumor necrosis factor-related protein 3 precursor  
DE (Secretory protein COR526).  
GN C1QTNF3 OR CTRP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Piddington C.S., Bishop P.;  
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RA Maeda T., Hayashi A., Saito T.;  
RT "Molecular cloning, chromosomal localization, and genomic structure of the human COR526 gene.";  
[3]  
RP Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
CC  
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CC -----  
CC EMBL; AF329837; AAK17961.1; -  
CC EMBL; AF326976; AAK70344.1; -  
CC EMBL; BC016021; AAH16021.1; -  
CC EMBL; BC016021; AAH16021.1; -  
CC EMBL; HGNC:14326; C1QTNF3.  
CC InterPro; IPR001073; C1q.  
CC InterPro; IPR000087; Collagen.  
CC Pfam; PF00386; C1q; 1.  
CC Pfam; PF01391; Collagen; 1.  
CC PRINTS; PR00007; COMPLEMENTC1Q.  
CC SMART; SM0110; C1q; 1.  
CC PROSITE; PS01113; C1q; 1.  
CC Collagen; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 246  
FT  
FT POTENTIAL.  
FT COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-  
FT RELATED PROTEIN 3.

DR	PROSITE; PS01113; ClQ; 1.
KW	Collagen signal.
FT	SIGNAL 16
CH	CHAIN 17 289
FT	POTENTIAL. COMPLEMENT-ClQ TUMOR NECROSIS FACTOR-RELATED PROTEIN 7.
FT	DOMAIN 38 139 COLLAGEN-LIKE.
FT	DOMAIN 141 276 CLQ.
SQ	SEQUENCE 289 AA; 30683 MW; A61609FF86D26946 CRC64;
Query Match 23.0%; Score 315; DB 1; Length 289; Best Local Similarity 30.1%; Pred. No. 1.3e-19; Matches 86; Conservative 32; Mismatches 96; Indels 72; Gaps 9;	
QY	14 LFLLPFLCQDEVMESPTGLPPDCSKCHGDSFRGYQGPGPPGGIPGNHGNGN 73   :
Dd	5 LYVTSFAICASGPRGNQLKGENSPRYIC-----SIFGLCPGPFGANGSGFPHGRIGL 60   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY	74 NGATGHEGAKEGD-----KGDLPGRGERGHQP--- 103       :
Dd	61 PGRDGRGRKGEKGTAGLRGTGLPLAGEKDQGETCKKGPIGPEGEKGVGP 120   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY	104 -----KGEKGYGPFP-----ELQIAFMASLIATHFSNQNSGIIPSSETNIGNFDV 150   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	121 PGPKGRDREGDGDPGLGVRGCGSVILKSASFVGITSTPYERLPFIINKVLNEGEHNP 180   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY	151 MTGFEGAPVSQVFYEFTSM--KHEDVEEYYVLMINGNTVFSMYSEMK-----GKS 201   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	181 ATGFICAFIGIYFYSDITLANKH-----LAIGLVNG-----QYRIKTFDANTGNH 228   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY	202 DTGSNHAVLKAKGDEVYLRM----GNGALHGDHQRFSTFAGFLLF 243   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Dd	229 DVASGSTVIVLOPEDEVWLIEFTTDQNLGFLSDPCGWADSLSFGLLY 274   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
RESULT 3	
CQT2_HUMAN	ID CQT2_HUMAN STANDARD; PRT; 285 AA.
AC	O9BXJ5;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Complement-clq tumor necrosis factor-related protein 2 precursor.
GN	CIQTAF2 OR CTBP2.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	piddington C.S., Bishop P.;
RP	"Homo sapiens complement-clq tumor necrosis factor-related protein.";
RL	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC	[2]
CC	SEQUENCE FROM N.A.
RC	TISSUE=Muscle;
RA	Strausberg R.;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC	- - SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC	- - SIMILARITY: CONTAINS 1 CLQ DOMAIN.
CC	----
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenses@isb-sib.ch). -----
Dd	EMBL; AF329836; AAA17960.1; -
Dd	EMBL; BC011699; AAA11699.1; -
Dd	Gene; HGNC:14325; CIQTNF2.
Dd	InterPro; IPR001073; Clq.
Dd	InterPro; IPR000087; Collagen.
CC	----







```
or send an email to license@lsb-sib.ch)
-----
CC EMBL; U37222; AAA80543.1; -
DR EMBL; U49915; AAB06706.1; -
DR EMBL; AF304466; AAK13417.1; -
DR EMBL; AK003138; BAB22597.1; -
DR MGD; MGI:106675; ACRP30.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PRO0007; COMPLEMENTC1Q.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;
KW Polymorphism.
FT SIGNAL 1 17
FT CHAIN 18 247
FT DOMAIN 45 110
FT DOMAIN 111 247
FT DISULFID 39 39
FT MOD_RES 47 47
FT MOD_RES 50 50
FT MOD_RES 56 56
FT MOD_RES 65 65
FT MOD_RES 79 79
FT MOD_RES 98 98
FT MOD_RES 107 107
FT VARIANT 113 113
FT CONFLICT 50 50
FT CONFLICT 74 74
FT CONFLICT 117 117
FT CONFLICT 148 148
FT CONFLICT 243 243
SQ SEQUENCE 247 AA; 26841 MW; 137B687D873988C4 CRC64;
Query Match 21.5%; Score 294; DB 1; Length 247;
Best Local Similarity 31.5%; Pred. No. 6.5e-18;
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;
Qy 6 LIYWOLLALFPLFCODEYMESPQTGG--LPPDCSKCHGYSFRGYGQPPGPPGPPG 63
Dy 2 LLLQALLPLLIP-SHAEDVTTTEELAPALVPPPKGTCA-----CWMA-----GIPG 48
Qy 64 IPGNHNGNNGATGCEKGEKGDGLGRGER---GQHGPKGEKYPGIPPE----- 115
Dy 49 HPCHNGTPTGRDGTGPKGEKGDAGLLGPKGETGDVGMTCAGEPGPGCTGPKRGEPG 108
Qy 116 -----LQIAFNASLATPNSQNSGIFFSVETNIGNFFDVTGRTGAPVSGVYFFTFSM 170
Dy 109 EAAVYRSFASVGLTRVTVNVPFRFKIFYNQONHYDGTGKPYCNPGLYFYSYHIT 168
Qy 171 KHEDVEEYVYLMHNGNTVFSMYEMKGSKDTSSNHAVLKLAKGDEYWLRM-GNG---A 226
Dy 169 VY--MKDVKVSLEFKDKAVLFTYDQYQEKNDQASGVLLHLEVDGQVWLQVYGDGDH 226
Qy 227 LHGDHORESTAGLLP 243
Dy 227 LYADNVNDSTFTGFLY 243
RESULT 7
ID APM1_HUMAN STANDARD; PRT; 244 AA.
AC Q15848;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adiponectin precursor (30 kDa adipocyte complement-related protein)
DE (ACRP30) (Adipose most abundant gene transcript 1) (apM-1) (gelatin-
DE binding protein).
GN APM1 OR ACRP30 OR GBP28.
OS Homo sapiens (Human).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=96224171; PubMed=8619847;
RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,
RA Matsubara K.;
RT "cDNA cloning and expression of a novel adipose specific collagen-like
RT factor, apM1 (Adipose Most abundant Gene transcript 1).";
RL Biochem. Biophys. Res. Commun. 221:286-289(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99196984; PubMed=10095105;
RA Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,
RA Nakano Y., Shimizu N., Tomita M.;
RT "Organization of the gene for gelatin-binding protein (GBP28).";
RL Gene 229:67-73(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99333693; PubMed=10403784;
RA Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,
RA Fuerst A., Schoelmerich J., Schmitz G.;
RT "The human apM-1, an adipocyte-specific gene linked to the family of
RT TNF's and to genes expressed in activated T cells, is mapped to
RT chromosome 1q21.3-q23, a susceptibility locus identified for familial
RT combined hyperlipidemia (FCH).";
RL Biochem. Biophys. Res. Commun. 260:416-425(1999).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=204117747; PubMed=10961870;
RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,
RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,
RA Matsuzawa Y.;
RT "Adiponectin, a new member of the family of soluble defense collagens,
RT negatively regulates the growth of myelomonocytic progenitors and the
RT functions of macrophages.";
RL Blood 96:1723-1732(2000).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=20440368; PubMed=10982546;
RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,
RA Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y.,
RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
RT "Adiponectin, an adipocyte-derived plasma protein, inhibits
RT endothelial NF-kappaB signaling through a CAMP-dependent pathway.";
RL Circulation 102:1296-1301(2000).
RN [6]
RP FUNCTION.
RX MEDLINE=21372498; PubMed=11479627;
RA Yamauchi T., Kamon J., Waki H., Terachi Y., Kubota N., Hara K.,
RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,
RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,
RA Froguel P., Kadowaki T.;
RT "The fat-derived hormone adiponectin reverses insulin resistance
RT associated with both lipotrophy and obesity.";
RL Nat. Med. 7:941-946(2001).
RN [7]
RP VARIANT ADIPONECTIN DEFICIENCY CVS-112.
RX MEDLINE=20378830; PubMed=10918532;
RA Takahashi M., Arita Y., Yamagata K., Matsukawa Y., Okutomi K.,
RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,
RA Yamashita S., Funahashi T., Matsuzawa Y.;
RT "Genomic structure and mutations in adipose-specific gene,
RT adiponectin.";
RL Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).
RN [8]
RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.
RX MEDLINE=21671103; PubMed=11812766;
RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,
RA Otabe S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y.,
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RA Yazaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,  
RA Kimura S., Tomita M., Kimura S., Ito C., Froguet P., Kadowaki T.,  
RT "Genetic variation in the gene encoding adiponectin is associated with  
an increased risk of type 2 diabetes in the Japanese population.",  
RL Diabetes 51:536-540(2002).  
CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE  
CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH  
CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING  
CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED  
CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE  
CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.  
CC -1- SUBUNIT: HOMODIGLIMER (POTENTIAL).  
CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.  
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.  
CC -1- DISEASE: Defects in AP1 are the cause of adiponectin deficiency,  
CC resulting in very low concentration of plasma adiponectin.  
CC Decreased adiponectin plasma levels are associated with obesity  
CC insulin resistance, and diabetes type 2.  
CC -1- PHARMACEUTICAL: Adiponectin might be used in the treatment of  
CC diabetes type 2 and insulin resistance.  
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
CC -----  
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CC -----  
DR EMBL; D45371; BAA08227.1; -;  
DR EMBL; AB012165; BAA86716.1; -;  
DR EMBL; AB012164; BAA86716.1; JOINED.  
DR EMBL; AJ131460; CAB52413.1; -;  
DR EMBL; AJ131461; CAB52413.1; JOINED.  
DR MIM; 605441; -;  
DR InterPro; IPR001073; C1q.  
DR InterPro; IPR000087; Collagen.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; PS01110; C1q; 1.  
DR SMART; PS01113; C1q; 1.  
DR Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;  
KW Polymorphism; Disease mutation; Obesity; Diabetes mellitus.  
FT SIGNAL 1 14 POTENTIAL.  
FT CHAIN 15 244 ADIPONECTIN.  
FT DOMAIN 42 107 COLLAGEN-LIKE.  
FT C1Q 108 244 C1Q.  
FT DISULFID 36 36 INTERCHAIN (BY SIMILARITY).  
FT MOD\_RES 44 44 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 47 47 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 53 53 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 62 62 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 71 71 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 76 76 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 86 86 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 95 95 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 104 104 HYDROXYLATION (BY SIMILARITY).  
FT VARIANT 84 84 G -> R.  
FT FTid=VAR\_013273.  
FT R -> C (IN ADIPONECTIN DEFICIENCY).  
FT FTid=VAR\_013274.  
FT V -> M.  
FT FTid=VAR\_013275.  
FT I -> T.  
FT FTid=VAR\_013276.  
FT R -> S.  
FT FTid=VAR\_013277.  
FT H -> P.  
FT FTid=VAR\_013278.  
FT SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;

Query Match 21.5%; Score 293.5; DB 1; Length 244;  
Best Local Similarity 34.5%; Pred. No. 7.1e-18;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;  
QY 53 QGP-----PGPPGP-----PGIPGNHGNNGNATGHEGAKGKGD---LGPR---GE 97  
Db 23 QGPVLLPLPKGACTGMWAGIPGPHGNHGNAPGRDPTGKGEKGDPLGPKGDIGE 82  
QY 98 RGQHGPKGEGYGI-----PPE-----LQIAPWASLATHFSNQNSGIISSVETNIGNF 147  
Db 83 TGVPGAEGPRGPGIOGRKGEPEGAYVYRSAFSGVLETVYTPNMPDRTKIFYNOONH 142  
QY 148 FDMVTGRFAPVSGVYFETSMKHEDEVEYVYLMHNGNTVFSMYEMKGRSDTSSNH 207  
Db 143 YDSTGKFNHICGLYFAHYIYV--MKDVKVSFLFKDKAMLFYDQYQENNVQASGS 200  
QY 208 AVILKAGDEWILRM-GNG---ALHGDHQRFTFAGFLF 243  
Db 201 VLLHLEVGQWLQVYGEGERNGLYADNDNDSTFTGFLY 240  
RESULT 8  
CQT6\_HUMAN STANDARD; PRT; 278 AA.  
ID CQT6\_HUMAN  
AC Q9BXI9;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement-c1q tumor necrosis factor-related protein 6 precursor.  
GN C1QTNF6 OR CTRP6.  
OS Homo sapiens (Human).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Piddington C.S., Sheppard P.O.;  
RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RC TISSUE=Placenta;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
CC -----  
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CC -----  
DR EMBL; AF329842; AAK17966.1; -;  
DR EMBL; BC020551; AAK20551.1; -;  
DR Genew; HGNC:14343; C1QTNF6.  
DR InterPro; IPR001073; C1q.  
DR InterPro; IPR000087; Collagen.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; PS01110; C1q; 1.  
DR PROSITE; PS01113; C1Q; FALSE\_NEG.  
KW Collagen; Signal.  
FT SIGNAL 1 46 POTENTIAL.  
FT CHAIN 47 278 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-  
FT DOMAIN 97 138 RELATED PROTEIN 6.  
FT DOMAIN 139 278 COLLAGEN-LIKE.  
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CONFLICT 21 21 G -> V (IN REF. 2).
SQ SEQUENCE 278 AA; 30861 MW; 27A82CA863F23D47 CRC64;

Query Match 21.2%; Score 289.5; DB 1; Length 278;
Best Local Similarity 28.8%; Pred. No. 1.8e-17;
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

QY 9 WQLALFELFCODEYMESPTGGLPPDCSKC-----
DB 29 WAALLLFL--WCEIPWELTDRVASQCRCOCSEDLDPAHVSSASSSRPHALPE 85
QY 49 FRGY-----QGPFGPPGPIGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHG 102
DB 86 IRPVINITILKDKDGPNGLPFGYMGREGPGQPGQSGKD-----
QY 103 PKCEGYPGIPPELQAFMA-----SLATHFSNQNSGIIFFSVETNIGNFDDYMTGRFGA 157
DB 129 -KGMGSPGAP--CQRFFAFSGVGRKTAHSGEDFOTLLFERVFNLDGCFDMATGQFAA 185
QY 158 PVSGVYFFTFPMKHE-DVEEVVYLMHNGNTVFSMYSYEMKCKSDTSSNHAVLKLAGD 216
DB 186 PLRGIYFFSLNV--HSNNYKETVTHMHNOKEAVILYA-OPSERSIMQSQSVMLDLAYGD 242
QY 217 EVNLRM-----GNGALHGDHQRSTFAGFL 242
DB 243 RVVRLFKRORENAIYNSDFDTVTTFSGHLI 273

RESULT 9
GLIC_MOUSE
ID GLIC_MOUSE STANDARD; PRT; 255 AA.
AC Q9ESN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Gliacolin precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20428709; PubMed=10862616;
RA Koide T., Aso A., Yorihuzi T., Nagata K.;
RT "Conformational requirements of collagenous peptides for recognition
RT by the chaperone protein HSP47."
RL J. Biol. Chem. 275:27957-27963(2000).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN GLIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 CIQ DOMAIN.
CC
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CC
DR EMBL; AB044560; BAB15806.1; -
DR InterPro; IPR001073; CIQ.
DR pfam; PF00386; CIQ; 1.
DR PRINTS; PR00007; Collagen; 1.
DR SMART; SMO0110; CIQ; 1.
DR PROSITE; PS01113; CIQ; 1.
KW Collagen; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 255 GLIACOLIN.
FT DOMAIN 61 111 COLLAGEN-LIKE.
FT DOMAIN 120 255 CIQ.
SQ SEQUENCE 255 AA; 26687 MW; 529FFBAF4B2191BC1 CRC64;

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Query Match 20.9%; Score 285.5; DB 1; Length 255;
Best Local Similarity 34.2%; Pred. No. 3.5e-17;
Matches 68; Conservative 32; Mismatches 82; Indels 17; Gaps 5;

QY 61 PPOIPNHNNGNNGATGHEGAKGKDGKDLGPRGERGQHGKPKGKGYGPIPELQIAF 120
DB 56 PTFIGPKGEAGRPGRGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPGPPG 114
QY 121 MASLATH-----FSNQNSG---IIFSSVETNIGNFDDYMTGRGAPVSGVYFFT 166
DB 115 ALSAATYSTVPKIAFYAGLKQRHGEYEVLFKFDVVTNLGNHNDPTTGKTCISPIGYFT 174
QY 167 FS-MMKHDEVEEYVYVLMHNGNTVFSMYSYEMKCKSDTSSNHAVLKLAGDEVLMRNG 225
DB 175 YHVLRRGGDGTSMWADLCKNNQVRASAIQAQADQNDYASNSVVLHLEPGDEVYIKLDG 234
QY 226 ALH-GDHQRSTFAGFLF 243
DB 235 KAHGNNKYSTFSGFIIY 253

RESULT 10
CALA_CHICK
ID CALA_CHICK STANDARD; PRT; 674 AA.
AC P08125;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Collagen alpha 1(X) chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.
RX MEDLINE=86168227; PubMed=3082876;
RA Ninomiya Y., Gordon M., van der Rest M., Schmid T., Linsenmayer T.,
RA Olsen B.R.;
RT "The developmentally regulated type X collagen gene contains a long
RT open reading frame without introns."
RL J. Biol. Chem. 261:5041-5050(1986).
RN [2]
RP SEQUENCE OF 1-75 FROM N.A.
RX MEDLINE=89054019; PubMed=2461368;
RA Luvallie P., Ninomiya Y., Rosenblum N.D., Olsen B.R.;
RT "The type X collagen gene. Intron sequences split the 5'-untranslated
RT region and separate the coding regions for the non-collagenous amino-
RT terminal and triple-helical domains."
RL J. Biol. Chem. 263:18378-18385(1988).
RN [3]
RP REVISIONS TO C-TERMINUS.
RX MEDLINE=89380199; PubMed=2476437;
RA Yanaguchi N., Benya P.D., van der Rest M., Ninomiya Y.;
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
RT demonstrate that type VIII collagen is a short chain collagen and
RT contains triple-helical and carboxyl-terminal non-triple-helical
RT domains similar to those of type X collagen."
RL J. Biol. Chem. 264:16022-16029(1989).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PYM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 CIQ DOMAIN.
CC
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FT CONFLICT 500 H -> L (IN REF. 3).
FT CONFLICT 567 A -> C (IN REF. 3).
FT CONFLICT 569 I -> H (IN REF. 3).
FT CONFLICT 571 FD -> IV (IN REF. 3).
FT CONFLICT 572 Q -> TV (IN REF. 3).
FT CONFLICT 635 O -> T (IN REF. 3).
SQ SEQUENCE 680 AA; 56775 MW; FE984CA99AF708E2 CRC64;

Query Match 20.4%; Score 278.5; DB 1; Length 680;
Best Local Similarity 30.5%; Pred. No. 4.1e-16;
Matches 73; Conservative 34; Mismatches 87; Indels 45; Gaps 7;

QY 45 GDYSFRGQGPCCPGPCIPGNGHNGNGATG-----HEGAKCEKDGKDGDLGPRGERG 99
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 GEGPIGTRGPGPCVCGFCGSKGDPGNPGAPGAGIATKGLNGPTGPPGPPGPRGHS 502
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 QHGPKGEKGYGPIIP-----PELQ-----IAFMASLATHF 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 503 EPLGEPGPCCPGPGQAYMPDGIKAGORPLSGMPLVSANHGVTGMPVSAFTVILSKAY 562
QY 129 SNQSGIIFSSVETNIGNFDVMTGRCFAGVSGVYFFETSMKKHEDVEEVVYLMHNGNT 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 563 PAVGAPIFDELYNRQOHYDPSRISFTCKTPIGYIFSIHV--HVKGTHVWVGLYKNGTP 620
QY 189 VFSWYSYE--MKGKSDTSSNHAVLKLAGDEVLWLMGN---GALHGHDQRSTFAGFL 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 621 --TWITYDEYSGYLDQAGSALMELTENDQWLQLPNAESNGLYSSEYVHSSFGFLV 677

RESULT 12
CALA_BOVIN
ID CALA_BOVIN STANDARD; PRT; 674 AA.
AC P23206;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Collagen alpha 1(X) chain precursor.
GN COL1A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
[1]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=Cartilage;
RA MEDLINE=9113131; Pubmed=1703407;
RA Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.;
RT "Isolation of cDNAs encoding the complete sequence of bovine type X
RT collagen. Evidence for the condensed nature of mammalian type X
RT collagen genes".
RL Biochem. J. 273:143-148(1991).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 CIQ DOMAIN.
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DR EMBL: X53556; CAA37624.1; -.
DR PIR: S13301; S13301.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.

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COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT  
C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1  
TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE  
FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.  
-|- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R  
AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED  
OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE  
A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF  
THE C CHAIN.  
-|- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
-|- SIMILARITY: CONTAINS 1 C1Q DOMAIN  
-----  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL: X66295; CAA46993.1; -  
DR EMBL: X92960; CAA63535.1; -  
DR PIR: S29328; S29328.  
DR MGI: 88225; C1qc.  
DR InterPro: IPR001073; C1q.  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF00386; C1q; 1.  
DR Pfam: PF01391; Collagen; 1.  
DR PRINTS: PR00007; COMPLEMENTC1Q.  
DR SMART: SM00110; C1Q; 1.  
DR PROSITE: PS01113; C1Q; 1.  
DR Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;  
KW Repeat; Signal.  
FT SIGNAL 1 29  
FT CHAIN 30 246 COMPLEMENT C1Q SUBCOMPONENT, C CHAIN.  
FT DOMAIN 32 113 COLLAGEN-LIKE.  
FT DOMAIN 114 246 C1Q.  
FT DISULFID 33 33 INTERCHAIN (WITH OTHER C CHAIN)  
FT (BY SIMILARITY).  
FT MOD\_RES 37 37 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 40 40 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 43 43 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 61 61 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 64 64 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 73 73 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 76 76 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 79 79 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 82 82 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 97 97 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 100 100 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 106 106 HYDROXYLATION (BY SIMILARITY).  
FT MOD\_RES 109 109 HYDROXYLATION (BY SIMILARITY).  
FT SEQUENCE 246 AA; 25966 MW; 2f79EA1274BCB8E0 CRC64;  
Query Match 30.0%; Score 274; DB 1; Length 246;  
Best Local Similarity 31.3%; Pred. No. 3.2e-16;  
Matches 71; Conservative 29; Mismatches 79; Indels 48; Gaps 7;  
Qy 51 GYQPPGPPGPPGIPGHNHNGNNGATGCH-----EGAKGEKGDGDLGRGEGHGPX 104  
Db 32 GCYIGPMGMPGAPGDGHDGLQGPGEPFPAVPTQGPQKQKQKGFPGHGRKNGPR 91  
Qy 105 GEKYPGIP-----PELQ-----IAFMASLATHFSNONSIIIFSSVETNIGNF 147  
Db 92 GTSGLPDGPPGPPGPPGEGYGRKQKQHSVFTVTRTTOYPEANALVRNSVVTNPQH 151  
Qy 148 FDMVTGRGAPVSGVYFFFTSMKHEDVEEYVYVLMNGNTVFSM-----YSYEMK 198  
Db 152 YNPSTGKFTCEVPGLYFVY-----YTSTANLCVHLNLRVASFCDHMF 198  
Qy 199 GKSDTSSNHAVLKAKDEWLRMG---NGALGHQHFSTFAGPLLF 243  
Db 199 NSKQVSSGALLRLQRGDEWVLSVNDINGMV-GIEGNSVFSGLLF 244

RESULT 14  
CA1A\_HUMAN  
ID CA1A\_HUMAN STANDARD; PRT; 680 AA.  
AC Q03692;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Collagen alpha 1(X) chain precursor.  
GN COL10A1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92109659; PubMed=1764025;  
RA Thomas J.T., Cresswell C.J., Rash B., Nicolai H., Jones T.,  
Solomon E., Grant M.E., Boot-Handford R.P.;  
RT "The human collagen X gene. Complete primary translated sequence and  
RT chromosomal localization.";  
RL Biochem. J. 280:617-623(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93012005; PubMed=1397333;  
RA Reichenberger E., Beier F., Luvallie P., Olsen B.R., von der Mark K.,  
Bertling W.M.;  
RT "Genomic organization and full-length cDNA sequence of human collagen  
RT X.";  
RL FEBS Lett. 311:305-310(1992).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Beier F., Lammi M.B., von der Mark K.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Williams S.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 52-680 FROM N.A.  
RX MEDLINE=92267014; PubMed=1567271;  
RA Apte S.S., Seidin M.F., Hayashi M., Olsen B.R.;  
RT "Cloning of the human and mouse type X collagen genes and mapping of  
RT the mouse type X collagen gene to chromosome 10.";  
RL Eur. J. Biochem. 206:217-224(1992).  
RN [6]  
RP SEQUENCE OF 561-666 FROM N.A.  
RX MEDLINE=91243838; PubMed=2037056;  
RA Apte S., Mattei M.-G., Olsen B.R.;  
RT "Cloning of human alpha 1(X) collagen DNA and localization of the  
RT COL10A1 gene to the q21-q22 region of human chromosome 6.";  
RL FEBS Lett. 282:393-396(1991).  
RN [7]  
RP SEQUENCE OF 547-655 FROM N.A.  
RX MEDLINE=92077285; PubMed=1743401;  
RA Reichenberger E., Aigner T., von der Mark K., Stoeb H., Bertling W.;  
RT "In situ hybridization studies on the expression of type X collagen  
RT in fetal human cartilage.";  
RL Dev. Biol. 148:562-572(1991).  
RN [8]  
RP REVIEW ON VARIANTS.  
RX MEDLINE=97255959; PubMed=9101290;  
RA Kuivaniemi H., Tromp G., Prockop D.J.;  
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
RT associated collagen (type IX), and network-forming collagen (type X)  
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
RL Hum. Mutat. 9:300-315(1997).  
RN [9]  
RP VARIANTS SMCD ASP-598 AND PRO-614.  
RX MEDLINE=94136476; PubMed=8304336;  
RA Wallis G.A., Rash B., Sweetman W.A., Thomas J.T., Super M., Evans G.,  
Grant M.E., Boot-Handford R.P.;





Db 537 TPLVSNQGVTPMPVSAFTVILSKAYPAIGTPIPEDKILYNROQHYDPRGTGFTQIPGI 596

QY 163 YFTTFEMKHEDVEEVYVILMHNGNTVFSMYSEMGKSDTSSNHAHLAKGDEVWLRM 222

Db 597 YPFSYHV--HVKGTHVMVGLKNGTVMYTYDEYTRKGLDQASGSAIIDLTENDQVWLQL 654

QY 223 GN--GALHGDHORESTFAGFL 242

Db 655 PNAESNGLYSSYVHSFSGFLV 677

RESULT 15

COT5\_HUMAN

ID COT5\_HUMAN STANDARD; PRT; 243 AA.

AC Q9BXJ0; Q9UFK4;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Complement-clq tumor necrosis factor-related protein 5 precursor.

GN C1QTNF5 OR CTRP5

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Sheppard P.O., Humes J.M.;

RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 25-243 FROM N.A.

RC TISSUE=Uterus;

RA Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,

RA Wiemann S.;

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

CC -----

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CC -----

DR EMBL; AF329841; AAK17965.1; -.

DR EMBL; AL110261; CAB53702.1; -.

DR Genew; HGNC:14344; C1QTNF5.

DR InterPro; IPR001073; C1q.

DR InterPro; IPR000087; Collagen.

DR Pfam; PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 1.

DR PRINTS; PR00007; COMPLEMENTC1Q.

DR SMART; SM01110; C1Q; 1.

DR PROSITE; PS01113; C1Q; FALSE\_NEG.

KW Collagen; Signal.

FT SIGNAL 1 15 POTENTIAL.

FT CHAIN 16 243 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-

FT RELATED PROTEIN 5.

FT DOMAIN 30 95 COLLAGEN-LIKE.

FT DOMAIN 97 243 C1Q.

SQ SEQUENCE 243 AA; 25298 MW; 7CCDA65CDA7EB784 CRC64;

Query Match 19.3%; Score 264.5; DB 1; Length 243;

Best Local Similarity 32.6%; Pred. No. 2e-15;

Matches 74; Conservative 35; Mismatches 93; Indels 25; Gaps 9;

QY 34 GLPP-DCSK--CCHGDYSFRGYGPPGPPGPGPGNHNNGNNGATGHEGAKGE--- 85

Db 15 GSPFLDNKTPSLCPG---HPGLPTGFGHGSQGLFGRDGRDGRDGPAPGKEGGRP 71

QY 86 --KGDGDLGRGERGQHGPKEKGYGPIPELQIAFMASLATHFSNQNSGIIFSSVETN 143

Db 72 GLPGRGDPGPRCEAGPAGPTGPGAGCSVPPRSFAFSAKRSESVPVPPSDAPLPFDRVLVN 131

QY 144 IGNFDDVMTGRFGAPVSGVYFFTFSSMKKHEDVEEVYV--LMHNGNTVFSMYSEMGK-- 199

Db 132 EQGHYDAVTGKFTCQVPGVYFAV---HATVYRASLQFDLVKNGESIASFFQF-FGGWP 186

QY 200 KSDTSSNHAHLAKGDEVWLRMNG--ALHGDHORESTFAGFL 243

Db 187 KPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDTSTFSGLVY 233

Search completed: January 13, 2003, 10:43:07

Job time : 14 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:41:03 ; Search time 33 Seconds  
(without alignments)  
1535.988 Million cell updates/sec

Title: -US-09-931-836-2  
Perfect score: 1367  
Sequence: 1 MLWRQLIYWQLLALFLPFC.....LHGDRFSTFAGLLFETK 246

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1311	95.9	246	11 Q9ES30	Q9es30 mus musculus
2	313	22.9	294	11 Q9B8U4	Q9b8u4 mus musculus
3	299	21.9	240	6 Q95WQ4	Q95wq4 bos taurus
4	293.5	21.5	243	6 Q95JD7	Q95jd7 macaca mula
5	276.5	20.2	675	6 Q9N178	Q9n178 sus scrofa
6	273	20.0	1077	4 Q8TE71	Q8te71 homo sapien
7	270	19.8	295	11 Q9Z1K4	Q9z1k4 rattus norv
8	266.5	19.5	158	4 Q9H667	Q9h667 homo sapien
9	258.5	18.9	705	4 Q8TE75	Q8te75 homo sapien
10	257.5	18.8	243	11 Q8R002	Q8r002 mus musculus
11	257.5	18.8	744	4 Q96D07	Q96d07 mus musculus
12	257	18.8	744	11 Q9B2V4	Q9b2v4 mus musculus
13	257	18.8	744	11 Q9Z1S8	Q9z1s8 mus musculus
14	247.5	18.1	194	6 Q95J95	Q95j95 canis famil
15	239.5	17.5	245	11 Q9DCM6	Q9dcm6 mus musculus
16	237.5	17.4	281	11 Q9QXP7	Q9qxp7 mus musculus

17	219.5	16.1	347	4 Q96IH6	Q96ih6 homo sapien
18	218	15.9	1017	11 Q99KA1	Q99ka1 mus musculus
19	216	15.8	2944	11 Q63870	Q63870 mus musculus
20	215	15.7	583	4 Q96G58	Q96g58 homo sapien
21	215	15.7	992	4 Q9UG76	Q9ug76 homo sapien
22	215	15.7	1016	4 Q9Y6C2	Q9y6c2 homo sapien
23	211	15.4	182	11 Q8R1P2	Q8r1p2 mus musculus
24	210.5	15.4	422	5 Q24893	Q24893 ephydatia m
25	207.5	15.2	1549	11 Q60444	Q60444 cricetus
26	203.5	14.9	673	4 Q14052	Q14052 homo sapien
27	197	14.4	171	13 Q90S86	Q90s86 gallus gall
28	195.5	14.3	1140	11 Q61434	Q61434 mus musculus
29	195.5	14.3	1774	11 Q62001	Q62001 mus musculus
30	194	14.2	224	5 Q9VVY2	Q9vvv2 drosophila
31	194	14.2	397	16 Q8XLT5	Q8xlt5 clostridium
32	191.5	14.0	594	5 Q9VEP4	Q9vep4 drosophila
33	190.5	13.9	289	5 Q62432	Q62432 caenorhabdi
34	190.5	13.9	890	5 Q77087	Q77087 alvinella p
35	190	13.9	476	13 Q9I8D5	Q9i8d5 gallus gall
36	189	13.8	292	11 Q9CS87	Q9csb7 mus musculus
37	189	13.8	375	4 Q8TCD8	Q8tcd8 homo sapien
38	188.5	13.8	187	11 Q9JHA9	Q9jha9 rattus norv
39	188.5	13.8	1745	4 Q9NZQ6	Q9nzz6 homo sapien
40	188	13.8	1344	13 Q93419	Q93419 gallus gall
41	187.5	13.7	680	11 Q9D0D2	Q9d0d2 mus musculus
42	185.5	13.6	303	5 Q23364	Q23364 caenorhabdi
43	185.5	13.6	1723	5 Q9G0B1	Q9gqb1 hydra atten
44	185	13.5	408	13 Q90604	Q90604 gallus gall
45	185	13.5	441	4 Q96A84	Q96a84 homo sapien

## ALIGNMENTS

## RESULT 1

Q9ES30 PRELIMINARY; PRT; 246 AA.  
AC Q9ES30  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Collageneous repeat-containing sequence of 26kda protein.  
GN CORC OR CORC26.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21264842; PubMed-11071891;  
RA Maeda T., Abe M., Kurisu K., Jikko A., Furukawa S.;  
RT "Molecular cloning and characterization of a novel gene, CORC26,  
RT encoding a putative secretory protein and its possible involvement in  
RT skeletal development.";  
RL J. Biol. Chem. 276:3628-3634(2001).  
DR EMBL; AF246265; AAC33704.1; .  
DR MGD; MGI:1932136; Corc.  
DR InterPro; IPR001073; Clq.  
DR InterPro; IPR000087; Collagen.  
DR Pfam; PF00386; Clq; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; SM00110; Clq; 1.  
DR PROSITE; PS01113; Clq; 1.  
SQ SEQUENCE 246 AA; 26828 MW; 42A481B3E9F48F7E CRC64;

Query Match 95.9%; Score 1311; DB 11; Length 246;  
Best Local Similarity 95.9%; Pred No. 9.2e-110;  
Matches 236; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MLWRQLIYWQLLALFLPFCQLQDEYMESPTQGGLPDCSKCHGDYSFRGQGGPPPG 60  
DB 1 MLGRQRIWHLPLFLPFCQLQDEYMESPTQGGLPDCSKCHGDYSFRGQGGPPPG 60

QY	61	PPGIPGNHNGNNGATGHEGAKGKGDGLPRGRGQHGPKGEGYGPPIPELQIAF	120
Db	61	PPGIPGNHNGNNGATGHEGAKGKGDGLPRGRGQHGPKGEGYGPPIPELQIAF	120
QY	121	MASLATHFSNQSGIIFSSVETNIGNFDVMTGREGAPVSGVYFFTFSMKHEDVEEYIV	180
Db	121	MASLATHFSNQSGIIFSSVETNIGNFDVMTGREGAPVSGVYFFTFSMKHEDVEEYIV	180
QY	181	YLMHNGNTVFSYMYEMKSDTSSNHAVLKAKGDEWLRMGALHGDHQRFSTFAGF	240
Db	181	YLMHNGNTVFSYMYETKSDTSSNHAVLKAKGDEWLRMGALHGDHQRFSTFAGF	240
QY	241	LFETK 246	
Db	241	LFETK 246	
RESULT 2			
ID	Q9D8U4	PRELIMINARY;	PRT; 294 AA.
AC	Q9D8U4;		
DT	01-JUN-2001 (T-REMBLrel. 17, Created)		
DT	01-JUN-2001 (T-REMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (T-REMBLrel. 17, Last annotation update)		
DE	1810033K05RIK protein.		
GN	1810033K05RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Barsh G.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK007683; BAB25187.1; -		
DR	MGI; MGI:1916433; 1810033K05RIK.		
DR	InterPro; IPR001073; Clq.		
DR	InterPro; IPR000087; Clq.		
DR	Pfam; PF00386; Clq; 1.		
DR	Pfam; PF01391; Collagen; 2.		
DR	PRINTS; PR00007; COMPLEMENTC1Q.		
DR	SMART; SM01110; C1Q; 1.		
DR	PROSITE; PS01113; C1Q; 1.		
SQ	SEQUENCE 294 AA; 30865 MW; 6D3905AE7C19E6FA CRC64;		
Query Match 22.9%; Score 313; DB 11; Length 294;			
Best Local Similarity 28.9%; Pred. No. 3.8e-20;			
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;			
QY	6	LIYWOLLALFFPLFCODEYN-----ESPQTGLPPDCSKCHGDSFRGYQGPGPP	59
Db	10	MISWILLAC-ALP---CAADPMGLAFARDFQKGFPQLVCS-----LFGPQGP	54

QY	61	PPGIPGNHNGNNGATGHEGAKGKGDGDLGPRGRCQHGPKEGYPGIPPELQIAF	120
Db	61	PPGIPGNHNGNNGATGHEGAKGKGDGDLGPRGRCQHGPKEGYPGIPPELQIAF	120
QY	121	MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFCAPVSGVYFFTFSMKKHEDVEEYV	180
Db	121	MASLATHFSNQNSGIIFSSVETNIGNFFDVMTGRFCAPVSGVYFFTFSMKKHEDVEEYV	180
QY	181	YLMHNGNTVFSMYSEYEMKGSKSDTSSNHAVLKAKGDEVWLRMGNGALHGHDHGRFSTFAGF	240
Db	181	YLMHNGNTVFSMYSEYEMKGSKSDTSSNHAVLKAKGDEVWLRMGNGALHGHDHGRFSTFAGF	240
QY	241	LLFETK 246	
Db	241	LLFETK 246	
RESULT 2			
ID	Q9DB04	PRELIMINARY;	PRT; 294 AA.
AC	Q9DB04;		
DT	01-JUN-2001 (Tremblrel. 17, Created)		
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)		
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)		
DE	1810033K05Rik protein.		
GN	1810033K05RIK		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Asakawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Buffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK007683; BAB25187.1; -		
DR	MGI; MGI:1916433; 1810033K05Rik.		
DR	InterPro; IPR001073; Clq.		
DR	InterPro; IPR000087; Collagen.		
DR	Pfam; PF00386; Clq; 1.		
DR	Pfam; PF01391; Collagen; 2.		
DR	PRINTS; PR00007; COMPLENNTCIQ.		
DR	SMART; SM0110; Clq; 1.		
DR	PROSITE; PS01113; Clq; 1.		
SQ	SEQUENCE 294 AA; 30865 MW; 6D3905AE7C1956FA CRC64;		
Query Match 22.9%; Score 313; DB 11; Length 294;			
Best Local Similarity 28.9%; Pred. No. 3.8e-20;			
Matches 86; Conservative 41; Mismatches 89; Indels 82; Gaps 12;			
QY	6	LIYWOLLALFLFPLCLCODEYM-----ESPQTGGLPPDCSKCHGDSYFRGYPGPPGPP	59
Db	10	MISWVLLAC-ALP---CAADPMLGAFARRDFQKGGPQLVCS-----LPGQGP	54

[illegible]

RESULT 5	Q9N178	PRELIMINARY;	PRT;	675 AA.
ID	Q9N178			
AC	Q9N178;			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Type X collagen.			
GN	COL10A1.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Sulina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21015405; PubMed=11130976;			
RA	Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,			
RA	Shukri N.M., Thomsen B.;			
RT	"Abnormal growth plate function in pigs carrying a dominant mutation			
RT	in type X collagen".			
RL	Mamm. Genome 11:1087-1092(2000).			
DR	EMBL; AF222861; AAF37271.1; -.			
DR	InterPro; IPR001073; Clq.			

DR	InterPro:	IPR000087; Collagen.
DR	Pfam:	PF00386; C1q; 1.
DR	Pfam:	PF01391; Collagen; 8.
DR	PRINTS:	PR00007; COMPLENNTC1Q.
DR	ProDom:	PD000007; Collagen; 2.
DR	SMART:	SM00110; C1Q; 1.
DR	PROSITE:	PS01113; C1Q; 1.
KW	Collagen.	
SQ	SEQUENCE	675 AA; 65447 MW; 26397B10310383F9 CRC64;
	Query Match	20.2%; Score 276.5; DB 6; Length 675;
	Best Local Similarity	32.0%; Pred. No. 1.9e-16;
	Matches 73; Conservative	27; Mismatches 87; Indels 41; Gaps 7;
QY	51	GYGQPPGPPGPPIGNHNNNGNATGHEG---AKGEKGDKGDLGP-----RGERGQH 102
Db	450	G'RGPG'GGIGPFGSGKDPCNPGRPAGIATKGLNGTGP'PGPGPKGHACEPLGP 509
QY	103	PKAGEGYDQ-I'PPELQIAFMASLATHSFNSQNQGII-----F 137
Db	510	PPGPGPPGQAVPPE---GFVKEGORAFVSANQVGTGMPSAFTVLSKAYPAIGAPIPF 566
QY	138	SVETNIGNFDVTMGREGAPVGSGVYFFTFFSMMKHEDVEEVVYLHMHGNTVFESMYSEM 197
Db	567	DKILYNGQQHYDPKTGI'FTCRIPGIYFSYHI--HVKCTHA'VGLYNGKTPVMYTYDEIV 624
QY	198	EKSDTSNNAVLKLAKGEVWLRM---GNCALGHDHQHFSTFAAGFL 242
Db	625	KGLDOAGSGAILDTNDNQWQLQPNAGSNGLYSSEYVHSFSGFLV 672

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RESULT 6
Q8TE71
ID Q8TE71 PRELIMINARY; PRT; 1077 AA.
AC AC
Q8TE71;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE EGG1.
OS EGG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
[1]
RN RN
RP SEQUENCE FROM N.A.
RA Aerobajnai W., Miller J.L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY074490; AAL71549.1; -
SQ SEQUENCE 1077 AA, 120974 MW: 2888BF3CA7D032D6 CRC64:

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Query Match	20.0%	Score 273;	DB 4;	Length 1077;
Best Local Similarity	29.6%	Pred. No. 7e-16;		
Matches	72;	Conservative 43;	Mismatches 90;	Indels 38; Gaps 8;
QY	34	GLPDCSKCCHGDIS	-----FRGYQGP	-----GPPGPPGIPGNHNGNN 74
Db	840	GLP	::: ::	::: ::
QY	75	GATCHEGAKGKDGDLGPRGBCG	-----HGPKGE	---KGYPGLPELQIAFMAS 123
Db	896	QVSSPE	-RDNETNSDCSGDSRSMTP	PVDPVTNPAATLPHVVP-LPQQMRVAFSA 953
QY	124	LATHFS	-NONSGIIFSSVTNIGNEFDVMT	GRGAPVSGVYFTFSMKMHEDVEVYV 181
Db	954	RTSLAPGTLDDPIVFDLLNNIGET	FDLQGRFCNPVCTYVF	IFHMLKLVANVPLYN 1013
QY	182	LMHNGNTVESMYEMKGRSDTS	SSNHAUCLKAGDEWFLRMNGAL	HGHQHFSTFAGPL 241
Db	1014	LMKNEEVLVSAYANDGAPDHET	ASNHAILQLFGQDIWLRHGA	IGYSSWYSTFSGL 1073
QY	242	LFE 244		
			::: ::	





```

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK018742; BAB31383.1; -.
DR MGD; MGI:88463; Col8a1.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 7.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;
Best Local Similarity 29.6%; Pred. No. 1.2e-14;
Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;

QY 34 GLPPDCSKCHGYDFRGYGGPPGPGPGPGIPGNHNGNNGATGHEGA-----KGE 85
DB 487 GIPGD--QGLQGGPIGIVGSPSIGPPGIPGPKGPGPLGPPGPGVAGLHGP 544
QY 86 KGDKGDLGPRGEGQHGKPKGKGVGPI-----PELQI----- 118
DB 545 PGKPGALGPOGQGLPGPPGPPGPPAVMPPTSPGGEYLPDMGLGIDGVKPPHAYAGK 604
QY 119 -----AFMASLATHFSNQNSGIIFSSVETNIGNFFDMVTCGRFGAPVSGYFFT 166
DB 605 KGKHGGPAYEMPAFTAELTPFPVPGAPVAFDKLLYNGRONYNPQTGIFTCEVPGVYIFA 664
QY 167 FSMKMHEDVEVYVLMHNGNTVFSMYSEMKGKSDTSSNHAHLKAKGDEVWLMRGN-- 224
DB 665 YHV--HCKGGNVWVAFKNEPMYTYDEYKKGFLDQASGSAVLLLRPGDOVFLQMPSEQ 722
QY 225 -GALHGDRHRETFAGFLLF 243
DB 723 AAGLYAGQYVHSSFSGYLLY 742

RESULT 14
Q95J95 PRELIMINARY; PRT; 194 AA.
ID Q95J95
AC Q95J95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Adiponectin (Fragment).
GN APM1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE TISSUE;
RA Kabir M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,
RA Dea M.K., Bergman R.N.;
RT "Regulation of Adiponectin gene expression in the fat-fed dog.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF417206; AAL09702.1; -.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR ProDom; PD000007; Collagen; 1.
DR PROSITE; PS01113; Clq; UNKNOWN_1.
FT NON_TER 1 194
FT NON_TER 194 194
SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;

Query Match 18.1%; Score 247.5; DB 6; Length 194;
Best Local Similarity 30.9%; Pred. No. 1.7e-14;
Matches 60; Conservative 36; Mismatches 71; Indels 27; Gaps 6;

QY 54 GP-----PGPPGP-----PGIPGNHNGNNGATGCHGAKGKDGKGD---LGPGRGGO- 100
DB 1 GPGVLLPLPKGACPGWMAGIPGHPGHGTPGRDGRDGTGPKGKGKGDGLVGFPGDGTGET 60
QY 101 --HGPKEGKGVGPIPEL-----QIAFMASLATHFSNQNSGIIFSSVETNIGNFF 148
DB 61 GVTGVEGPRGPGTPGPKGPGESAYVHRSFVSGLESRTITVPNVPTRFTKIFYNLQNH 120
QY 149 DVMTGREGAPVSGYFFTFSSMKHEDVEVYVLMHNGNTVFSMYSEMKGKSDTSSNHA 208
DB 121 DGTGKFKHCNIPGLYFESYHITVY--LKDVKVSILYKADKAMLFYDQYQEKNVDAQSGV 178
QY 209 VLKAKGDEVWLMR 222
```

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK018742; BAB31383.1; -.
DR MGD; MGI:88463; Col8a1.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 7.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM00110; Clq; 1.
DR PROSITE; PS01113; Clq; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Query Match 18.8%; Score 257; DB 11; Length 744;
Best Local Similarity 29.6%; Pred. No. 1.2e-14;
Matches 77; Conservative 27; Mismatches 102; Indels 54; Gaps 6;

QY 34 GLPPDCSKCHGYDFRGYGGPPGPGPGPGIPGNHNGNNGATGHEGA-----KGE 85
DB 487 GIPGD--QGLQGGPIGIVGSPSIGPPGIPGPKGPGPLGPPGPGVAGLHGP 544
QY 86 KGDKGDLGPRGEGQHGKPKGKGVGPI-----PELQI----- 118
DB 545 PGKPGALGPOGQGLPGPPGPPGPPAVMPPTSPGGEYLPDMGLGIDGVKPPHAYAGK 604
QY 119 -----AFMASLATHFSNQNSGIIFSSVETNIGNFFDMVTCGRFGAPVSGYFFT 166
DB 605 KGKHGGPAYEMPAFTAELTPFPVPGAPVAFDKLLYNGRONYNPQTGIFTCEVPGVYIFA 664
QY 167 FSMKMHEDVEVYVLMHNGNTVFSMYSEMKGKSDTSSNHAHLKAKGDEVWLMRGN-- 224
DB 665 YHV--HCKGGNVWVAFKNEPMYTYDEYKKGFLDQASGSAVLLLRPGDOVFLQMPSEQ 722
QY 225 -GALHGDRHRETFAGFLLF 243
DB 723 AAGLYAGQYVHSSFSGYLLY 742

RESULT 13
Q921S8 PRELIMINARY; PRT; 744 AA.
ID Q921S8
AC Q921S8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011061; AAH11061.1; -.
DR MGD; MGI:88463; Col8a1.
DR InterPro; IPR001073; Clq.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 7.
DR PROSITE; PS01113; Clq; UNKNOWN_1.
KW Collagen.
SQ SEQUENCE 744 AA; 73621 MW; BF7A7FD79D8463AA CRC64;
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 13, 2003, 10:42:54 ; Search time 10 Seconds  
(without alignments)  
477.266 Million cell updates/sec

Title: US-09-931-836-2

Perfect score: 1367

Sequence: 1 MLWRQLIYWQLLALFLPFC.....LHGDHQRFSTAGFLLETK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1367	100.0	246	9	US-10-036-041-2
2	1367	100.0	246	12	US-10-036-342-2
3	294	21.3	247	10	US-09-776-976-4
4	294	21.5	247	10	US-09-758-055-4
5	294	21.5	247	10	US-09-909-547-4
6	293.5	21.5	244	9	US-09-911-1768-48
7	293.5	21.5	244	10	US-09-776-976-6
8	293.5	21.5	244	10	US-09-758-055-6
9	293.5	21.5	244	10	US-09-909-547-6
10	293	21.4	247	10	US-09-776-976-2
11	293	21.4	247	10	US-09-758-055-2
12	293	21.4	247	10	US-09-909-547-2
13	290.5	21.3	259	9	US-09-989-293A-47
14	290.5	21.3	259	9	US-09-989-735-47
15	290.5	21.3	259	9	US-09-989-444-47
16	290.5	21.3	259	9	US-09-989-730-47
17	290.5	21.3	259	9	US-09-990-436-47
18	290.5	21.3	259	9	US-09-991-181-47
19	290.5	21.3	259	9	US-09-991-181-47

20	290.5	21.3	259	9	US-09-993-687-47	Sequence 47, Appl
21	290.5	21.3	259	9	US-09-989-734-47	Sequence 47, Appl
22	290.5	21.3	259	10	US-09-989-722-47	Sequence 47, Appl
23	290.5	21.3	259	10	US-09-989-723-47	Sequence 47, Appl
24	290.5	21.3	259	10	US-09-989-279-47	Sequence 47, Appl
25	290.5	21.3	259	10	US-09-989-727-47	Sequence 47, Appl
26	290.5	21.3	259	10	US-09-989-731-47	Sequence 47, Appl
27	290.5	21.3	259	10	US-09-989-732-47	Sequence 47, Appl
28	290.5	21.3	259	10	US-09-991-073-47	Sequence 47, Appl
29	290.5	21.3	259	10	US-09-991-073-47	Sequence 47, Appl
30	290.5	21.3	259	10	US-09-991-163-47	Sequence 47, Appl
31	290.5	21.3	259	10	US-09-993-604-47	Sequence 47, Appl
32	290.5	21.3	259	10	US-09-990-456-47	Sequence 47, Appl
33	290.5	21.3	259	10	US-09-989-721-47	Sequence 47, Appl
34	290.5	21.3	259	12	US-10-052-586-62	Sequence 62, Appl
35	289.5	21.2	278	10	US-09-799-777-35	Sequence 35, Appl
36	287	21.0	247	9	US-09-911-1768-3	Sequence 3, Appl
37	273	20.0	746	9	US-09-854-133-185	Sequence 185, App
38	273	20.0	746	10	US-09-738-973-185	Sequence 185, App
39	264.5	19.3	243	9	US-09-944-413-42	Sequence 42, Appl
40	264.5	19.3	243	9	US-09-944-403-42	Sequence 42, Appl
41	264.5	19.3	243	9	US-09-944-896-42	Sequence 42, Appl
42	264.5	19.3	243	9	US-09-944-944-42	Sequence 42, Appl
43	264.5	19.3	243	9	US-09-944-907-42	Sequence 42, Appl
44	264.5	19.3	243	9	US-09-944-929-42	Sequence 42, Appl
45	264.5	19.3	243	9	US-10-028-072-362	Sequence 362, App

## ALIGNMENTS

## RESULT 1

US-10-036-041-2  
; Sequence 2, Application US/10036041  
; Publication No. US20020192751A1  
; GENERAL INFORMATION:  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3030RIC8  
; CURRENT APPLICATION NUMBER: US/10/036,041  
; PRIOR FILING DATE: 2001-12-26  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/112514  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113300  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/113430  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113605  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/114140  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/115552  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/116843  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/125774  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/125778  
; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 2
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-036-041-2
Query Match 100.0%; Score 1367; DB 9; Length 246;
Best Local Similarity 100.0%; Pred. No. le-111; Indels 0; Gaps 0;
Matches 246; Conservative 0; Mismatches 0;
Qy 1 MLWRQLIYWQLLALFFLPCLCQDEYMESPTGGLPPDCSKCHGDYSFRGYQGPPGPPG 60
Db 1 MLWRQLIYWQLLALFFLPCLCQDEYMESPTGGLPPDCSKCHGDYSFRGYQGPPGPPG 60
Qy 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKCYGCGIPPELOIAF 120
Db 61 PPGIPGNHGNNGNNGATGHEGAKGKDGKDLGPRGERGQHGPKGKCYGCGIPPELOIAF 120
Qy 121 MASLATHFSNQSGLIFFSSVEINIGNFEDVMTGREGAPVSGVYFFTFSSMKHEDVEEYV 180
Db 121 MASLATHFSNQSGLIFFSSVEINIGNFEDVMTGREGAPVSGVYFFTFSSMKHEDVEEYV 180
Qy 181 YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKEDEWLRMGNGALHGDHORESTFAGF 240
Db 181 YLMHNGNTVFSMYSYEMKGKSDTSSNHAVLKLAKEDEWLRMGNGALHGDHORESTFAGF 240
Qy 241 LLFETK 246
Db 241 LLFETK 246
RESULT 2
US-10-036-342-2
; Sequence 2, Application US/10036342
; Patent No. US20020090681A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030RIC5
; CURRENT APPLICATION NUMBER: US/10/036,342
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113621  
 ; PRIOR FILING DATE: 1998-12-23  
 ; PRIOR APPLICATION NUMBER: 60/114140  
 ; PRIOR FILING DATE: 1998-12-23  
 ; PRIOR APPLICATION NUMBER: 60/115552  
 ; PRIOR FILING DATE: 1999-01-12  
 ; PRIOR APPLICATION NUMBER: 60/116843  
 ; PRIOR FILING DATE: 1999-01-22  
 ; PRIOR APPLICATION NUMBER: 60/125774  
 ; PRIOR FILING DATE: 1999-03-23  
 ; PRIOR APPLICATION NUMBER: 60/125778  
 ; PRIOR FILING DATE: 1999-03-23  
 ; PRIOR APPLICATION NUMBER: 60/125826  
 ; PRIOR FILING DATE: 1999-03-24  
 ; PRIOR APPLICATION NUMBER: 60/127035  
 ; PRIOR FILING DATE: 1999-03-31  
 ; PRIOR APPLICATION NUMBER: 60/127706  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 60/129122  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: 60/130359  
 ; PRIOR FILING DATE: 1999-04-21  
 ; PRIOR APPLICATION NUMBER: 60/131270  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: 60/131272  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: 60/131291  
 ; PRIOR FILING DATE: 1999-04-27  
 ; PRIOR APPLICATION NUMBER: 60/132371  
 ; PRIOR FILING DATE: 1999-05-04  
 ; PRIOR APPLICATION NUMBER: 60/132379  
 ; PRIOR FILING DATE: 1999-05-04  
 ; PRIOR APPLICATION NUMBER: 60/132383  
 ; PRIOR FILING DATE: 1999-05-04  
 ; PRIOR APPLICATION NUMBER: 60/135750  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: 60/138166  
 ; PRIOR FILING DATE: 1999-06-08  
 ; PRIOR APPLICATION NUMBER: 60/144791  
 ; PRIOR FILING DATE: 1999-07-20  
 ; PRIOR APPLICATION NUMBER: 60/146970  
 ; PRIOR FILING DATE: 1999-08-03  
 ; PRIOR APPLICATION NUMBER: 60/162506  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: 09/311832  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: 09/380142  
 ; PRIOR FILING DATE: 1999-08-25  
 ; PRIOR APPLICATION NUMBER: 09/644848  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 09/747259  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: 09/816744  
 ; PRIOR FILING DATE: 2001-03-22  
 ; PRIOR APPLICATION NUMBER: 09/854208  
 ; PRIOR FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: 09/854280  
 ; PRIOR FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: 09/874503  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: 09/869599  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: 09/908,827  
 ; PRIOR FILING DATE: 2001-07-18  
 ; PRIOR APPLICATION NUMBER: PCT/US99/10733  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: PCT/US99/28551  
 ; PRIOR FILING DATE: 1999-12-02  
 ; PRIOR APPLICATION NUMBER: PCT/US99/30720  
 ; PRIOR FILING DATE: 1999-12-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05601  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02  
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: PCT/US00/15264  
 ; PRIOR FILING DATE: 2000-06-02  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522  
 ; PRIOR FILING DATE: 2000-08-23  
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678  
 ; PRIOR FILING DATE: 2000-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956  
 ; PRIOR FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520  
 ; PRIOR FILING DATE: 2001-02-28  
 ; PRIOR APPLICATION NUMBER: PCT/US01/17800  
 ; PRIOR FILING DATE: 2001-06-01  
 ; PRIOR APPLICATION NUMBER: PCT/US01/19692  
 ; PRIOR FILING DATE: 2001-06-20  
 ; PRIOR APPLICATION NUMBER: PCT/US01/21066  
 ; PRIOR FILING DATE: 2001-06-29  
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735  
 ; PRIOR FILING DATE: 2001-07-09  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SEQ ID NO 2  
 ; LENGTH: 246  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-036-342-2  
  
 Query Match 100.0%; Score 1367; DB 12; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 1e-111;  
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 MLWRQLIYWQLLALFLPFLCQDEYMESQTGGLPDCSKCCCHGDSYFRGYGPPGPPG 60  
 Db 1 MLWRQLIYWQLLALFLPFLCQDEYMESQTGGLPDCSKCCCHGDSYFRGYGPPGPPG 60  
 Qy 61 PPGIPGNHNGNNGATGHEGAKGDKGDLGPRGERGOGHPKRGKGYGPIPELQIAF 120  
 Db 61 PPGIPGNHNGNNGATGHEGAKGDKGDLGPRGERGOGHPKRGKGYGPIPELQIAF 120  
 Qy 121 MASLATHFSNONGSIIFSSVETNIGNFDMTGRFAPVSGVYFFTFSMKMHEDVEEYV 180  
 Db 121 MASLATHFSNONGSIIFSSVETNIGNFDMTGRFAPVSGVYFFTFSMKMHEDVEEYV 180  
 Qy 181 YLMHNGNTVFSMYSEYEMKGSDDTSSNHAVALKLAKGDEWLMRGMGALHGDHQRSTFAGF 240  
 Db 181 YLMHNGNTVFSMYSEYEMKGSDDTSSNHAVALKLAKGDEWLMRGMGALHGDHQRSTFAGF 240  
 Qy 241 LLFETK 246  
 Db 241 LLFETK 246  
  
 RESULT 3  
 US-09-776-976-4  
 ; Sequence 4, Application US/09776976  
 ; Patent No. US20020037849A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fruebis, Joachim  
 ; APPLICANT: Erickson, Mary Ruth  
 ; APPLICANT: Yen, Frances  
 ; APPLICANT: Bihain, Bernard  
 ; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
 ; FILE REFERENCE: 76.US4.REG  
 ; CURRENT APPLICATION NUMBER: US/09/776,976  
 ; CURRENT FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/758,055  
 ; PRIOR FILING DATE: 2001-01-10  
 ; PRIOR APPLICATION NUMBER: US 60/176,228  
 ; PRIOR FILING DATE: 2000-01-14  
 ; PRIOR APPLICATION NUMBER: US 60/198,087

Db 49 HPGHNGTPGRDRGTGCEKGEKGDAGLLGPKGTGDMGTGAGPRGPGTGTGCRKGEPC 108  
Qy 116 -----LOIAFMA SLATHFSNQNSGIIFFSSVETNIGNFDVMTGRFGAPVSGVYFFTFMSM 170  
Db 109 EAAVMYRSFVSGLETRVTPNVPFRFTKIFYNQNHVDGSGTKFYCNIPGLYFVSHT 168  
Qy 171 KHEDEVEEYVYLMHNGNTVFSMYEMKGSDDTSSNNAVLKLAGDEWLM-GNG---A 226  
Db 169 VY--MKDVKSLEKDKAVLFTYDQYQEKNDQASGVLLHLEVGQDQVWLQVYGDGSHNG 226  
Qy 227 LHGDHQRSTFAGFLF 243  
Db 227 LYADNVNDSTFTGFLY 243

RESULT 5  
US-09-909-547-4  
; Sequence 4, Application US/09909547  
; Patent No. US20020091080A1  
; GENERAL INFORMATION:  
; APPLICANT: Fruebis, Joachim  
; APPLICANT: Erickson, Mary Ruth  
; APPLICANT: Yen, Frances  
; APPLICANT: Bihain, Bernard  
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
; FILE REFERENCE: 76.US6.CIP  
; CURRENT APPLICATION NUMBER: US/09/909,547  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 09/776,976  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: US 09/758,055  
; PRIOR FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: US 60/299,881  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: US 60/198,087  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: US 60/176,228  
; PRIOR FILING DATE: 2000-01-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: mus musculus  
US-09-909-547-4

Query Match 21.5%; Score 294; DB 10; Length 247;  
Best Local Similarity 31.5%; Pred. No. 1.5e-18;  
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

Qy 6 LIYWQLLALFFLPCLCODEYMESPTGG--LPPDCSKCHGDYSGRFGYGGPRGPPGP 63  
Db 2 LLLQALLFLILP-SHAEDDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48  
Qy 64 IPGNHNGNNGATGHEGAKGKGDGLGRGER---GOHGPKEGKGYGPIPE----- 115  
Db 49 HPGHNGTPGRDRGTGCEKGEKGDAGLLGPKGTGDMGTGAGPRGPGTGTGCRKGEPC 108  
Qy 116 -----LOIAFMA SLATHFSNQNSGIIFFSSVETNIGNFDVMTGRFGAPVSGVYFFTFMSM 170  
Db 109 EAAVMYRSFVSGLETRVTPNVPFRFTKIFYNQNHVDGSGTKFYCNIPGLYFVSHT 168  
Qy 171 KHEDEVEEYVYLMHNGNTVFSMYEMKGSDDTSSNNAVLKLAGDEWLM-GNG---A 226  
Db 169 VY--MKDVKSLEKDKAVLFTYDQYQEKNDQASGVLLHLEVGQDQVWLQVYGDGSHNG 226  
Qy 227 LHGDHQRSTFAGFLF 243  
Db 227 LYADNVNDSTFTGFLY 243

RESULT 6  
US-09-911-176B-48

Query Match 21.5%; Score 294; DB 10; Length 247;  
Best Local Similarity 31.5%; Pred. No. 1.5e-18;  
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

Qy 6 LIYWQLLALFFLPCLCODEYMESPTGG--LPPDCSKCHGDYSGRFGYGGPRGPPGP 63  
Db 2 LLLQALLFLILP-SHAEDDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48  
Qy 64 IPGNHNGNNGATGHEGAKGKGDGLGRGER---GOHGPKEGKGYGPIPE----- 115  
Db 49 HPGHNGTPGRDRGTGCEKGEKGDAGLLGPKGTGDMGTGAGPRGPGTGTGCRKGEPC 108  
Qy 116 -----LOIAFMA SLATHFSNQNSGIIFFSSVETNIGNFDVMTGRFGAPVSGVYFFTFMSM 170  
Db 109 EAAVMYRSFVSGLETRVTPNVPFRFTKIFYNQNHVDGSGTKFYCNIPGLYFVSHT 168  
Qy 171 KHEDEVEEYVYLMHNGNTVFSMYEMKGSDDTSSNNAVLKLAGDEWLM-GNG---A 226  
Db 169 VY--MKDVKSLEKDKAVLFTYDQYQEKNDQASGVLLHLEVGQDQVWLQVYGDGSHNG 226  
Qy 227 LHGDHQRSTFAGFLF 243  
Db 227 LYADNVNDSTFTGFLY 243

RESULT 4  
US-09-758-055-4  
; Sequence 4, Application US/09758055  
; Patent No. US20020058617A1  
; GENERAL INFORMATION:  
; APPLICANT: Fruebis, Joachim  
; APPLICANT: Erickson, Mary Ruth  
; APPLICANT: Yen, Frances  
; APPLICANT: Bihain, Bernard  
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
; FILE REFERENCE: 76.US4.REG  
; CURRENT APPLICATION NUMBER: US/09/758,055  
; CURRENT FILING DATE: 2001-01-10  
; PRIOR APPLICATION NUMBER: US 60/176,228  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: US 60/198,087  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: US 60/299,881  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: mus musculus  
US-09-758-055-4

Query Match 21.5%; Score 294; DB 10; Length 247;  
Best Local Similarity 31.5%; Pred. No. 1.5e-18;  
Matches 81; Conservative 40; Mismatches 102; Indels 34; Gaps 9;

Qy 6 LIYWQLLALFFLPCLCODEYMESPTGG--LPPDCSKCHGDYSGRFGYGGPRGPPGP 63  
Db 2 LLLQALLFLILP-SHAEDDVTTTEELAPALVPPPKGTCA-----GWMA-----GIPG 48  
Qy 64 IPGNHNGNNGATGHEGAKGKGDGLGRGER---GOHGPKEGKGYGPIPE----- 115

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; Sequence 48, Application US/09911176B
; Patent No. US20020156243A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ANTIBODIES THAT BIND AN
; ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
; FILE REFERENCE: 97-30D1
; CURRENT APPLICATION NUMBER: US/09/911,176B
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/118,408
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 60/053,154
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-176B-48

Query Match          21.5%; Score 293.5; DB 9; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKGDGKGD---LGPR---GE 97
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DB 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDGPGGLIGPKGDIGE 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 98 RGQHGPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQNSGIFFSVETNIGNF 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 TGVPGAEGPRGPGIOGRKGEPEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 FDMVTGRFGAPVSGVYFFFTFSMMKHEDVEVYVYLMHNGNTVFSMYSEMKGKSDTSSNH 207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFSTFAGFLIF 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
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RESULT 7
US-09-776-976-6
; Sequence 6, Application US/09776976
; Patent No. US20020037849A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.USA.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-776-976-6

Query Match          21.5%; Score 293.5; DB 10; Length 244;
Best Local Similarity 34.5%; Pred. No. 1.7e-18;
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

QY 53 QGP-----PGPPGP-----PGIPGNHNGNNGATGHEGAKGKGDGKGD---LGPR---GE 97
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DB 23 QGPGVLLPLPKGACTGWMAGIPGHPGCHNGAPGRDGTTPGKEGKGDGPGGLIGPKGDIGE 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 98 RGQHGPKGKGYPGI-----PPE-----LQIAFMASLATHFSNQNSGIFFSVETNIGNF 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 TGVPGAEGPRGPGIOGRKGEPEGAYVYRSFVGLTYVTIPNPIRFTKIFYNQNH 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 148 FDMVTGRFGAPVSGVYFFFTFSMMKHEDVEVYVYLMHNGNTVFSMYSEMKGKSDTSSNH 207
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DB 143 YDGTGKFKHCNIPGLYFYFAYHTIVY--MKDVKVSFLFKDKKAMLFYDQYQENNVDAQSGS 200
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QY 208 AVLKLAGDEWLRM-GNG---ALHGDHORFSTFAGFLIF 243
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DB 201 VLLHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240
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RESULT 9
US-09-909-547-6
; Sequence 6, Application US/09909547
; Patent No. US20020091080A1
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
```

US-09-909-547-6

Query Match 21.5%; Score 293.5; DB 10; Length 244;  
Best Local Similarity 34.5%; Pred. No. 1.7e-18;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US6.CIP  
CURRENT APPLICATION NUMBER: US 09/909,547  
CURRENT FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 09/776,976  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/758,055  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 6  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-909-547-6

Query Match 21.5%; Score 293.5; DB 10; Length 244;  
Best Local Similarity 34.5%; Pred. No. 1.7e-18;  
Matches 76; Conservative 35; Mismatches 78; Indels 31; Gaps 9;

APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US6.CIP  
CURRENT APPLICATION NUMBER: US 09/909,547  
CURRENT FILING DATE: 2001-07-19  
PRIOR APPLICATION NUMBER: US 09/776,976  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/758,055  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 6  
LENGTH: 244  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-776-976-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US4.REG  
CURRENT APPLICATION NUMBER: US 09/776,976  
CURRENT FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/758,055  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 2  
LENGTH: 247  
TYPE: PRT  
ORGANISM: mus musculus

US-09-776-976-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US4.REG  
CURRENT APPLICATION NUMBER: US 09/776,976  
CURRENT FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: US 09/758,055  
PRIOR FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 2  
LENGTH: 247  
TYPE: PRT  
ORGANISM: mus musculus

US-09-758-055-2

Sequence 2, Application US/09758055  
Patent No. US2002003849A1  
GENERAL INFORMATION:  
APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US4.REG  
CURRENT APPLICATION NUMBER: US 09/758,055  
CURRENT FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 2  
LENGTH: 247  
TYPE: PRT  
ORGANISM: mus musculus

US-09-758-055-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

APPLICANT: Erickson, Mary Ruth  
APPLICANT: Yen, Frances  
APPLICANT: Bihain, Bernard  
TITLE OF INVENTION: OB3 Globular Head and Uses Thereof for Decreasing Body Mass  
FILE REFERENCE: 76.US4.REG  
CURRENT APPLICATION NUMBER: US 09/758,055  
CURRENT FILING DATE: 2001-01-10  
PRIOR APPLICATION NUMBER: US 60/176,228  
PRIOR FILING DATE: 2000-01-14  
PRIOR APPLICATION NUMBER: US 60/198,087  
PRIOR FILING DATE: 2000-04-13  
PRIOR APPLICATION NUMBER: US 60/299,881  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent.pm  
SEQ ID NO 2  
LENGTH: 247  
TYPE: PRT  
ORGANISM: mus musculus

QY 226 --ALHGDHQRSTFAGFLF 243  
 Db 224 HNGLYADNVNDSTFTGFLF 243

RESULT 12  
 US-09-547-2  
 ; Sequence 2, Application US/09909547  
 ; Patent No. US20020091080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Erickson, Joseph  
 ; APPLICANT: Erickson, Mary Ruth  
 ; APPLICANT: Yen, Frances  
 ; APPLICANT: Blahm, Bernard  
 ; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass  
 ; FILE REFERENCE: 76.056.CIP  
 ; CURRENT APPLICATION NUMBER: US/09/909,547  
 ; CURRENT FILING DATE: 2001-07-19  
 ; PRIOR APPLICATION NUMBER: US 09/776,976  
 ; PRIOR FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: US 09/758,055  
 ; PRIOR FILING DATE: 2001-01-10  
 ; PRIOR APPLICATION NUMBER: US 60/239,881  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: US 60/198,087  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR APPLICATION NUMBER: US 60/176,228  
 ; PRIOR FILING DATE: 2000-01-14  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2  
 ; LENGTH: 247  
 ; TYPE: PRT  
 ; ORGANISM: mus musculus  
 US-09-909-547-2

Query Match 21.4%; Score 293; DB 10; Length 247;  
 Best Local Similarity 31.2%; Pred. No. 1.9e-18;  
 Matches 81; Conservative 40; Mismatches 99; Indels 40; Gaps 10;

QY 6 LIYWQLLALFFFLCQDEYEWSPQTGG--LPPDCSKCHGDYSFRGYGPPGPPG 63  
 Db 2 LLQALFLFLID-SHAEDDVTTTELAPALVPPKGTCA-----GNA-----G 45

QY 64 IPGNHNGNNGATGHEGAKGKDGDD--LGPRGER--GQHPKGEKGYGTPPE-- 115  
 Db 46 IPGSHGHNCTPGRDGDTGPEKGEKGSCLLPKGTGCVMTGAEGRGPPTGPRKG 105

QY 116 -----LQIAFMASLATHFNSQNSGIIFSVETNIGNFFDVMTRGFCAPVSGVYFFTF 167  
 Db 106 EPGEAAVYRSGFVSGLETRVTPVNPVIRFTKIFYNQNHNDSTGKFCNIPGLYYSF 165

QY 168 SMKKHDEVEVYVYLHNGNNTVFESYEMKCKSDTSSNHAHLKLAKGDEWLRM-GNG- 225  
 Db 166 HITVY--MKDVVSLFKKDKAVLFYDQYQEKNVDAQSGSVLLHLEVGDDQVWLVYGGDD 223

QY 226 --ALHGDHQRSTFAGFLF 243  
 Db 224 HNGLYADNVNDSTFTGFLF 243

RESULT 13  
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 ; Sequence 47, Application US/09992598  
 ; Patent No. US20020160384A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone

;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
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;; PRIOR APPLICATION NUMBER: 60/091360  
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;; PRIOR APPLICATION NUMBER: 60/091478  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
Query Match 21.3%; Score 290.5; DB 9; Length 259;  
Best Local Similarity 28.8%; Pred. No. 3.2e-18; Indels 63; Gaps 10;  
Matches 78; Conservative 34; Mismatches 96;  
QY 9 WQLLALFLLPFCLODHYMESPTGGTGLPPDCSKCC-----HGDS 48  
Db 10 WAALLLFL---MCEIRVELITDRAVASCQCCDSEDPDPAHVSSASSSGRPHALPE 66  
QY 49 FRGY-----QGGPPGPPGPGIGNHNNGNNGATGHEGAKGKGDGLGPRGERGOH 102  
Db 67 IRPYINITILKDGKDPGPMGLPGYMGREGPGQGPQSKGD----- 109  
QY 103 PKGEGYGPGLPELQIAFMA-----SLATHFSNQNSGIIFFSSVETNIGNEFDVMTGRFA 157  
Db 110 -KGEWGSPGAP--CQKRFFAFSVGRKTAHSGEDFQTLIFERFVNLDCGCFDNGTQFAA 166  
QY 158 PVSGVYFFTFMSMKHE--DVEEVYVYLMHNGNTVFSMTSYEMKGSDFSSNHAULKLAGD 216  
Db 167 PLRGIYFFSLNV--HSWNYKETIYVHMHNOKEAVILYA--OPSERSIMQSOSVMLDLAYGD 223  
QY 217 EWLIRM-----GNGALHGDHQRFTFAGFL 242  
Db 224 RVWVRLFKRQRENAIYSNDFDTYITFSGLI 254  
RESULT 14  
US-09-989-293A-47



; Sequence 47, Application US/09989293A  
; Patent No. US2002017164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P27301C66  
; CURRENT APPLICATION NUMBER: US/09/989,293A  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
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; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/087106  
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Query Match      21.3%; Score 290.5; DB 9; Length 259;
Best Local Similarity 28.8%; Pred No. 3.2e-18;
Matches 78; Conservative 34; Mismatches 96; Indels 63; Gaps 10;

QY      9  WOLLALFLPCLCODEYMESPQTGGLPDPCSKCC-----HGDS 48
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Db      10  WAALLLELL---MCEIRVELFTEDRAVAGCQRCCDSELDPAHVSSASSGRPHALPE 66
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QY      49  FRGY-----QQPPGPGPGPIPNHGNNNGNNGATGHEGAKGEKDGDLGPRGQHG 102

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Mon Jan 13 10:56:36 2003

Db 67 IRPYINITLKGDGPGMGLPGYMGREGPGQEGPQGSKG----- 109  
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Db 110 -KGEMSGPGAP--CORRFFAFSVGRKTAHSGEDFQTLFFRVFNLDGCFDMATGQFAA 166  
QY 158 PVSGVFFFTFSMMKHE-DVEEVYVYLMHNGNTVFSMSYEMKGSQSDTSSNHA VLKLAGD 216  
Db 167 PLRGIYFFSLNV--HSWNYKETVYVHMHNQKEAVILYA-QPSERSIMOSQSVMLDLAYGD 223  
QY 217 EWLRM-----GNGALHGDHQRFTFAGELL 242  
Db 224 RVWVRLFKRQRENAIYSNDFDTYITFSGHLI 254

Search completed: January 13, 2003, 10:44:51  
Job time : 11 secs